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Result
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Listing first 45 summaries
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   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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638	403	578	343	518	283	458	223	398	165	338	105	278	45	218	y Ma Loc thes	Note: DKE	rime	s-re	cule	98510	ted	SSIO	ies:	netic	н_
RQYFELQCRQYKRKMLLARHSLDQDLLREDLNKKQTQKDLECALLLRQHEATRELELRQL 697		LAALLEAQKRTYKLRKEQLKEELQENPSTPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQ 637	EREEHSARLQRELEAQRAGFGAEAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKE 402	EREEHSGRIQRELEAQRAGFGTEAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKE 577	RRAYCRNRDHFATIRTASLVSRQIQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRG 342	RRAYCRNRDHFATIRTASLVSRQIQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRG 517	AREMAMMQEGEHTVTSHSSIIHRLPGSDNLYDDPYQPEITPSPLQPPAAPAPTSTTSSAR 282	SREMAMMQEGEHTVTSHSSIIHRLPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSAR 457	YMHRAGTLTSLESSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEEEEEGPE 222	YMHRAGTLTSLESSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEGPE 397	HRFVLRERPPTVIMDLIQRTKDAVRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEP 164	HRFVLRERPPTVIMDLIQRTKDAVRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEP 337	VÄERKPPLFUNMAMSALYHIAQNESPVLQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLK 104	LAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLK 277	Query Match 68.7%; Score 3530; DB 2; Length 1062; Best Local Similarity 90.8%; Pred. No. 1.4e-97; Matches 695; Conservative 24; Mismatches 40; Indels 6; Gaps 3;	Note: DKFZp434N1427.1	Experimental source: adult testis; clone DKFZp434N1427	A;Residues: I-1062 <aaa> A;Cross-references: EMBL:AL137701</aaa>	Molecule type: mRNA	Accession: T46444	submitted to the Protein Sequence Database, January 2000  A; Reference number: Z23032	B . Moude B . Carronhuhor I .	<pre>C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000</pre>	T46444 hypothetical protein DKFZp434N1427.1 - human	
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C; Function:
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A;Residues: 1-1001 <HUT>
A;Cross-references: EMBL:AF084205; NID:g3452472; PID:g3452473; PIDN:AAC71014.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Isolation of TAO1, a protein kinase that activates A;Reference number: Z18730; MUID:99003202; PMID:9786855 A;Accession: T17365 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hutchison, M.; Berman, K.S.; Cobb, M.H. J. Biol. Chem. 273, 28625-28632, 1998 A;Title: Isolation of TAO1, a protein kin
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C;Date: 1717365
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                  ASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEEEFFESREMAMMQEGEHTVTSHSSIIHR 420
                                                                                  VRELDNIQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRAGTLTSLESSHSVPSMSIS 360
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                                                                                                                                                ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA 300
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ASSQSSSVNSLPDASDDKSELD--
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                                                               VRELDNLQYRKMKKLLFQEAHNGPAVEAQEEEEEQDHGGGRTGTVNSVGSNQSIPSMSIS
                                                                                                                                 ESPTLQSNEWSDYFRNFVDSCLQKIPQDRPTSEELLKHMFVLRERPETVLIDLIQRTKDA
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MMEGDHTVMSNSSVIHL
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RESULT 3
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A; Map position: 3
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A; Residues: 1-982 <BAR>
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A; Accession: T18576
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                                                   RAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LASQERNIIGQEEAGAWNLWEKEH--GNLVDMEFK-----LGWVQGPV-----L 895
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SNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQE 125
                                   KPGVIKDPSIAALFSNKDPEQRYQDLREIGHGSFGAVYFAYDKKNEQTVAIKKMNFSGKQ 67
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                                                                                                    27.6%; Score 1416.5; I
ilarity 34.8%; Pred. No. 2e-35;
Conservative 162; Mismatches 3
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serine/threoine protein kinase - guinea pig
N;Alternate names: STE20-like kinase
C;Species: Cavia porcellus (guinea pig)
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 21-Jul-2000
C;Accession: T18532
R;Itoh, S.; Kameda, Y.; Yamada, E.; Tsujikawa, K.; Mimura, T.; Kohama, Y.
Arch. Blochem. Blophys. 340, 201-207, 1997
A;Reference number: Z18952; MUID:97288344; PMID:9143322
A;Accession: T18532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLGSEKKKKQYEHVKRDLNPEEFWETIGELGDGAFGKVYKAQNKETNVLAAAKVID---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAGSLKDPDVAELFFKD-DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGK
                  KGEQEKELS - - :
                                               LGQQKKELAALLEAQKRTYKLRKEQLKEELQENPSTPKREKAEWLLRQKEQLQQCQAEEE
                                                                                                                                                 QKKTLKKTRKFIVDGVEVSVTTSKIVTDSDSKTEELRFLRRQELRELRFLQKEEQRAQQQ
                                                                                                                                                                                                                                                                                 RGAPMAVTQMDTEKNETPHEAPAQVEVQVPVPPQPSEPPPAPIPSININSEAAENKGEMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIQTVDLVSQETGEKEVDIHILDSEVVHAVEDTHEKLRKDDTTQKDVISDTSSVGERDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPESREMAMMQEGEHTVTSH---SSIIH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIMDLIQRTKDAVRELDNLQYRKMKKI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANSFYGTPYWMAPEVIL--AMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTESQIQVVCKQTLEALNYLHDNKITHRDLKAGNILFTLDGDIKLADFGVSAKNTRTIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQEVEIAAVIHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLYKLGDFG----SASIMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSEEELEDYMVEIDILASCDHPNIVKLLDAFYYENNLWILIEFCAGGAVDAVMLEL-ERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSNEKWQDIIKEYRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKP
                                                                                  LNGKLQQQREQIFRRFEQEMMSKKRQYDQEIENLEKQQKQTIERLEQEHTNRLRDEAKRI
                                                                                                          HSGRLQRELEAQRAGFGTEAEKLARRH-QAIGEKEARAAQAEERKFQQH------I
                                                                                                                                                                                                                  ASLNTETILLPESESQKENDTDSGTGSTADNSSIDLNLSISSFLSKTKDNGSISLQETRR
                                                                                                                                                                                                                                                  ATIRTASLV --- SRQIQEHEQDSA-----
                                                                                                                                                                                                                                                                                                                                                  KLVENTHEKQLPISSETTLDTSEGLGASEGREVTESGSTEEVEVEGAVSETDEEDVQSET
                                                                                                                                                                                                                                                                                                                                                                                   IGAVPKTAESSAEGAQGDGGKETDEGAQILISKATEGPKASGTEEAPPVTEITETNDTDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTLTSLESSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEEE-----EEEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEHNASGDKFSTKVLNEKPCPGEPENAVELVGGAVAVLPDRATELPESGREEKRPKLDR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKAEVTEEVEDGKEEDDDEEIENSLPIPTNKRASSDLSIASSEEDKLSQNACILESVSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAKSEPPTLAQPSRWSSNFKDFLKKCLEKNVDARWTTSQLLQHPFVTIDSNKPIRELIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAQNESPAL-QSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDSFIGTPYWMAPEVVMCETSKDRPYDYKADVWSLGITLIEMAEIEPPHHELNPMRVLLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- LPDTEDQEMADINSVSEGEEDHAVTSETNIEHNLKPEKERDQEKQPVLENKLVKSEDT
                                                                                                                                                                                                                                                                                                                  -DNLYDDPYQPEM-TPGPLQPPAAPPTSTSSSSARRAYCRNRDHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%;
22.3%;
                 -KFQNILKNRKKEVLNEVEKAPKDLRKELMKRRKEELAQSQHVQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 663; DB 2;
Pred. No. 3.7e-13;
6; Mismatches 372;
                                                                                                                                                                                                                                                                                                                                                                                    ----GS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -MRRQHQKQLLALESRLRGEREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1231;
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probable serine/threonine kinase F23010.20 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cross) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: B96716

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-836 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F23010.20
ILFQEAPNGPGAEAPEEEEEAEPYMHRAGTLTSLESSHSVPSMSISASSQSSSVNSL---
                                                                                                                                                                                                                                                                                                                                       REDPTTKYEFLNELGKGSYGSYYKARDLKTSEIVAVKVISLT--EGEEGYEEIRGEIEML
                                                        HDFVAKCLTKEPRLRPTAAEMLKHKFV--
                                                                                       RNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELDNLQYRKMKK
                                                                                                                                                           AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYF
                                                                                                                                                                                               AYLHSIYKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVI- 418
                                                                                                                                                                                                                              AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSAS----IMAPANSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                   QQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVADLMNVTEEALEEYQIAYICREALKGL
                                                                                                                                                                                                                                                                                                    QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
                                                                                                                                                                                                                                                                                                                                                                         KDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-RELELRQLQAVQR-
                                                                                                                          --QENRYDGKVDVWALGVSAIEMAEGLPPRSSVHPMRVLFMISIEPAPMLEDKEKWSLVF
                                                                                                                                                                                                                                                                                                                                                                                                                159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LKELDEEHSQELKEWR-EKLRPRKKTL---EEEFARKLQEQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIWELEERHLQEKHQLLKQQLKDQYFMQRHQLLK-RHEKETEQMQRYNQRLIEELKNRQT
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GB:AE005173; NID:g7705100; PIDN:AAF67779.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 662.5; DB 2;
Pred. No. 2.8e-13;
83; Mismatches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----TRAELTRLQHQTELGNQLEYNKRREQELRQKHA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KEGTTLEPEEQRILQEEMGTFSSSPQKHRS
                                                    -ERCKTGASAM-SPKIEKSRQ 522
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                                                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Khaykin, E.; Kim, C
Maiti, R.; Marziali
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C;Accession: T30989
R;Su, Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y.
EMBO J. 16, 1279-1290, 1997
A;Title: NIK is a new Ste20-related kinase that binds NI
A;Reference number: Z20954; MUID:97280817; PMID:9135144
A;Accession: T30989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1233 <SUY>
A; Cross-references: EMBL:UE
C; Keywords: protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               serine/threonine protein kinase NIK - mouse
N;Alternate names: Nck interacting kinase
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                             EHSGRLQRELEAQRAGFGTEAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAA 580
Q----RRRLEEQQ-----RREREARRQQ---EREQRRREQEEKR
                                                                                                                                      --NRDHFATIRTASLVSRQIQEHEQDSALREQLSGYKRMRRQHQKQLLA-LESRLRGERE
                                                                                                                                                                                                                              EGEHTVTSHSSIIHRLPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSARRRAYCR--
                                                                                                                                                                                                                                                                                                           TSLESSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEGPESREMAMMQ 405
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                                                                                                                                                                                      EGE----PSSIVN-VPGESTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTVGRRNTFIGTPYWMAPEVI-ACDENPDATYDYRSDLWSCGITAIEMAEGGPPLCDMHP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --MAPANSFVGTPYWMAPEVILAMDE---GQYDGKVDVWSLGITCIELAERKPPLFNMNA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDEEEEITLEINMLKKYSHHRNIATYYGAFIKKSPPGHDDQLWLVMEFCGAGSITDLVKN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEKWQDIIKEVRFLQKL-RHPNTIQYRGCYLR-----EHTAWLVMEYC-LGSASDLLEV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKSLVDIDLSSL----RDPAGIFELVEVVGNGTYGQVYKGRHVK-TVTAAIKVMDV----T 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: U88984; NID: g1872545; PID: g1872546; PIDN: AAC53165.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 651.5; DE Pred. No. 8e-13; 1; Mismatches 2
                                                                                                                                                                                                                                                                            --EYSGSEEEEEEVPE-----Q
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                                                                                      EEYKRQLLAERQKRIEQQKE
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YQ Y	റ	AQKRTYKLRKEQLKEELQENPSTPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQRQY      :   :	
Δb	· w	;	
Ωу	641 467	FELQCRQYKRKMLLARHSLDQDLLREDLNKKQTQKDLECALLLRQH 686   :  :	
Qy	687		
Вb	511	QDRSKPSFHAPEPKPHYDPADRAREVQWSHLASLKNNVSPVSRSHSFSDPSPKFAHHHLR 570	
Qy	727	EQELRQKHAAQVRQQPKSLKVRAGQLPMGLPATGALGP 764	
Вb	571	SQDPCPPSRSEGLSQSSDSKSEVPEPTQKAWSRSDSDEVPPRVPVRTTSRSPVLSRRDSP 630	
ОУ	765	LSTGTLSEEQPCSSGQEAILGQRMLGEEEEAVPERMILGKEGTTLEP 811	
Db	631	LOGGGQQNSQAGQRNSTSSIEPRLLWERVEKLVPRPGSGSSSGSSNSGSQPGSHPGSQSG 690	
Qy	812	EEQRILQEEMGTFSSSPQKHRSLVNEEDWDISKEMKESRVPSLASQERNI- 861	
Вb	691	RFRVRSSSKSEGSPSPRQESAAKKPDDKKEVFRSLKPAGEVDLT	
Qy	862	GAWNLWEKEHGNLVDMEFKLGWVQGPVLTPVPEEEEEEEEE	
DЬ	748	DVRPPHKVTDYSSSSEESGTTDEEEEDVEQE 778	
Qy	910	GAPIGTPRD 918	
Db	779	GADDSTSGPED 789	
RESULT 7 T14157 T24157 Serine/threon C;Species: Mu C;Date: 20-Se C;Accession: R;Pytowski, E	JT 7 57 scies: cies: ce: 20 sessic	ine protein kinase - mouse is musculus (house mouse) p-1999 #sequence_revision 20-Sep- T14157 .; Hicklin, D.J.; Kornhaber, G.;	
submitted A; Referen A; Accessi A; Status:	erencessic	the EMBL Data Library, December 1997 umber: Z17894 T14157 Tilminary; translated from GB/EMBL/DDBJ	
A; Mol A; Res A; Cro	A; Molecule t A; Residues: A; Cross-refe	Le type: mRNA es: 1-1233 <pyt> references: EMBL:AF039574; NID:g2773155; PID:g2773156; PIDN:AAB96682.1</pyt>	
Query Best Match		Match 12.5%; Score 643; DB 2; Length 1233; ocal Similarity 21.8%; Pred. No. 1.4e-12; ndels 442; Gaps 43;	
ду	6 11	RAGSIKDPDVAELFFKD-DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGK 64 :	
Qу	68	QSNEKWQDIIKEVRFLQKLRHDNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKP 122 :   : :  :   :           : :   :   :	
Qу ДЪ	123 127	LQEVBIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAP 178	
ОУ	179 187	ANSFYGTPYWMAPEVILAMDEGQYDGKYDYWSLGITCIELAERKPPLFNMNAMSALYH 236 	
Qy	237	NESPAL-QSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTV	
OV Db	247 294	AKSEPPTLAQPSKWSSNEKDELRKCLEKNVDARWTTSQLLQHPEVTVDSNKPVREL 30 ORTKDAVRE	
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06 EE 907	Ωу 90
** REDRY*EJMASQERNILIGGEAGAWNIMEREHG-NIPUMERKIGMYQGFYLTFYYEEEEEEE	Db 1139
DQDR	<u> </u>
7 RMLGEEEBAVPERNILGKEGTTLEPEEQRILQEEMGTFSSSPQKHRSLVNEEDWDISKEM	Оу 787
S KNRQTQERARLPKIQRSEAKTRMAMFKKSLRINSTATP	Db 105
731 RQKHAAQVRQQPKSLKVRAGQLPMGLPATGALGPLSTGTLSEEQPCSSGQEAILGQ	Qy 7
)O RAREAAIWELEERHLQEKHQLLKQQLKDQYFMQRHQLLK-RHEKETEQMQRYNQRLIEEL	Db 1000
684 ROHEAT-RELELROLQAVQRTRAELTRLQHQTELGNQLEYNKRREQEL	Оу б
54 QHAQEQEFYQKQQQELDGSLKKIIQQQKAELANIERECLNNKQQ-	Db 9
'26 QAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLDQDLLREDLNKKQTQKDLECALLL	Оу б
901 EAKRIKGEQEKELSKFQNVLKNRKKEVMNEVEKAPRELRRELTK-	Db 9
ALLEAQKRTYKLRKEQLKEE	Ωу 5
::: : :  ::             ::: 3 QQQLNGKLQQQREQIFRRFEQEMLSKKRQY	
519 REEHSGRLORELEAORAGFGTEAEKLARRHOAIGEKEARAAOAEERKFOOH-	Qy 5
490 LREQLSGYKR	Qy 4 Db 7
23 EMGALPKPETILPPEPEHEKGNDTDSGTGSTVENSSGDLNLSISSFLSKAKDSGSVSLQE	Db 7
67 HFATIRTASLVSRQIQEHE	Qy 4
664 IGSEGEAAATEVDLERKENAQKVPVKAESQAPAASQPSEPHPVLIPSININSET-TENKE	Db 6
423 -GSDNLYDDPYQPE-MTPGPLQPPAAPPTSTSSSSARRRAYCRNRD	Oy 4
604 DKQPEQQPAVCEAEGQLTSTSETTRATLEQPETDEVEQVSESNSIEELERLVVTGAEARA	Db 6
393 EEGPESREMAMMQEGEHTVTSHSSIIHRLP	Оу з
44 EVGTDEALDDTQKAAELSKAAQSGEGDEALVPTQTLAEKPTEGPEAGGAEEEPPGGERVE	Db 5
352 HSVPSMSISASSQSSSVNSLADASDNEEE	Ωу з
: :	
333 EEAEPYMHRAGT	Оу з
424 KRPKLENLPDTQDQQTVDVNSVSEENENNRVTLETNTDCLKPEEDRNKENQETLESKLIQ	Db 4
328APEEE	Оу з
364 SERTEQSTSEDKFSNKILNEKPTTDGPEKAVDEHASDVNLETGAELNDQTVG	Db 3
08 QYRKMKKILFQEAPNGPGAE	Оу з
304 IAEAKAEVTEEVEDGKEEDEEEEAENALPIPANKRASSDLSIASSEEDKLSQNACILESV	Db 3

RESULT 8
T34021
T34021
Protein kinase SK2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

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Db
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A;Residues: 1-1206 <FUX>
A;Residues: 1-1206 <FUX>
A;Cross-references: EMBL:AB003357; NID:d1106513; PID:d1020890; PIDN:BAA20077.1
A;Experimental source: Strain SD
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T34021
R;Fukami, Y.; Yamamoto, H.; Ichihara, T.; Mori, K.; Gomi, T.; Sato, K. submitted to the EMBL Data Library, April 1997
A;Description: SK2, a putative rat homologue of yeast protein kinase NRK1.
A;Reference number: Z21463
A;Recession: T34021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
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Best Local Similarity 21.3
Matches 258; Conservative
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784 TRRQKKTLKKTRKFIVDGVEVSVTTSKIVTDSDSKTEELRFLRRQELRELRLLQKEEQKA 843
                                456 -ARRRAYCRNRDHF-----ATIRTASLVSRQIQEHEQDSALREQ-LSGYKRMRRQHQKQ 507
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                                                                                                                                     QALGSKGEAATELDLEREENAQELPVKAEPQAPAASQASEPPPVLIPSINIHSENTENKG 723
                                                                                                                                                                       ---GS-----DNLYDDPYQPE-MTPGPLQPPAAPP------
                                                                                                                                                                                                                                                                             TSEVGTDEPPGDTQKSAEQSQDAEGGAGEEAPEPAQTLTEKATEGPEAHGAEEEPRSGER 603
                                                                                                                                                                                                         VEDKQLEQQSAVCEGEGQVTSTSESTRATTEEPETDEVDQVSESNSIEELERLGVTGAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEHNTSGDKFSNKVLSEKPTPEGPEKTVDVDGPANDVNLETVAEPNDQAVGFHENGREKK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---NLOYRKMKKILFQEAPNGPGAEAPEE-----EEEAEPY----MHRAGTLIS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAQNESPAL-QSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFV-----LRERPPT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSFYGTPYWMAPEVIL--AMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYH 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAGSLKDPDVAELFFKD-DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGK 64
                                                                EMGALPKPETILPPEPENGKGNDTDSGTGSTVENSSSDLNLSISSFLSKTKDSGSVSLQE 783
                                                                                                                                                                                                                                             -----REMAMMQEGEHTVT-------SHSSIIHRLP-----
                                                                                                                                                                                                                                                                                                               -----EGPES-----
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21.3%; Pred. No. 4.6e-12;
ative 162; Mismatches 326;
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Оу 258	Qy 198 Db 188	Qy 142 Db 131	Qy 83 Db 73	Qy 23 Db 15	Query Ma Best Loc Matches	A;Cross-re A;Experime C;Superfam C;Keywords F;18-270/D	A; Accession A; Molecule A; Residues	A;Title: A A;Referenc	C;Accessio R;Pombo, C	C;Species: C;Date: 29	RESULT 9 S71886	Db 1169	Оу 783	Db 1128	Qу 723	Оу 691 Db 1068	Db 1008	Оу 655	Db 954	Оу 614	894	568	844	Qу 508
VDSCLQKIPQDRPTSEVLLKHRFVLR-ERPPTVIMDLIQRTKDAVRELDNLQYRKMKKIL 316	DEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF 257 :                         :::      :	LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVILAM 197         :   :     :         :  ::  :  :	LRHDNTIQYRGCYLREHTAWLYMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141 	DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82    :  :	Query Match 11.5%; Score 592; DB 2; Length 426; Best Local Similarity 36.4%; Pred. No. 2e·11; Matches 154; Conservative 69; Mismatches 128; Indels 72; Gaps 16;	A;Cross-reterences: EMML:X99325; NLD:g1430821; PIDN:CAA6//00.1; PID:g1430822 A;Experimental source: cell type B cell cycle cyc		EMBO J. 15, 4537-4546, 1996 A;Title: Activation of a human Ste20-like kinase by oxidant stress defines a novel A;Reference number: S71886; MUID:97042345; PMID:8887545		Procesn kinase - numan Homo sapiens (man) -Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jul-2000		: :       EVFFKMTGESE 1179	ILGQRMLGEEE 793	ETQKLKELDEEHSQELKEWREKLRPRKKTLEEEFARKLQEQ 1168	NKRREQELRQKHAAQVRQQPKSLKVRAGQLPMGLPATGALGPLSTGTLSEEQPCSSGQEA 782	ELELRQLQAVQRTRAELTRL-QHQTELGNQLEY 722	KRHEKETEQMQRYNQRLIEELKNRQTQERARLPKIQRSEAKTRMAMFKKSLRINSTATPD 1067	ARHSLDQDLLR690	LANIERECLNNKQQLLRAREAAIWELEERHLQEKHQLLKQQLKDQYFIQRHQLL 1007	WILROKEOLOOCQAEEEAGILRRQROYFELQCROYKRKMIL 654	:	LOENPSTPKREKAE	QQQLNGKLQQQREQIFRRFEQEMLSKKRQYDQEIENLEKQQKQTIERLEQ 893	LLALESRLRGEREEHSGRLQRELEAQRAGFGTEAEKLARRHQAIGEKEARAAQAEERKFQ 567

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s: nucleic acid sequence not shown ule type: DNA ules: 1-1102 <pre> ues: 1-1102 <pre> ues: 1-1102 <pre> imental source: third instar eye-antennal disk cosmid l the cited accession number, 1076485, is not in Genbank ics: msn rds: phosphotransferase  Match Local Similarity 23.9%; pred. No. 4.3e-11; es 241; Conservative 124; Mismatches 293; Indels li : : : : : : : : : : : : : : : : : : :</pre></pre></pre>	ann, J.E.; Ito, N.; Rubin, G.M.  imisshapen encodes a protein kinase involved in cell sence number: JC6316; MUID:97199378; PMID:9047354  sion: JC6316  si: nucleic acid sequence not shown  le type: DMA  les: 1-1102 <tre> Intental source: third instar eye-antennal disk cosmid letype: DMA  les: phosphotransferase  Match  Matc</tre>	ttein kinase (EC 2.7.1) - fruit fly (Droso) prosophila melanogaster JC6316 JE: Ito, N; Rubin, G.M. 9-125, 1997  9-125, 1997  9-126, 1997  shapen encodes a protein kinase involved in number: JC6316; MUID:97199378; PMID:9047354 JC6316 JC631	d::HOG EOO baadaaa GO
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402 LOQOQOQANAANAANAHAAQQAQAAQQORAAQQBEEGAGLIRRORYFELGER 601 QENPSTPKREKAEWLL		a a	
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2::	11.4%; Score 585; DB 2; Length 690; 28.4%; pred. No. 4.6e-11; vative 110; Mismatches 243; Indels 135; Gaavyfardvrnsevvalkkmsysgkosnekwodlikev avyfardvrnsevvalkkmsysgkosnekwodlikev	ELTRLC STGTL: QQP QQP SSSSPQI :	ELAALLEAQKRTYKLRKEQLKEEL :  :: :: :: QANRQPKPPSRQQVEE

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R; Bentley, D.; Le, T.T.

R; Bentley, D.; Le, T.T.

submitted to the EMBL Data Library, April 1996

submitted to the EMBL Data Library, April 1996

A; Description: The sequence of C. elegans cosmid

A: Reference number: Z20614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein ZC404.9 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                  A;Map position: 5
A;Introns: 36/2; 82/2; 103/1; 131/3; 520/3; 622/2; 796/2
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U55363; PIDN:AAA97966.1; GSPDB:GN00023; CESP:ZC404.9 A;Experimental source: strain Bristol N2; clone ZC404. C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-829 <BEN>
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                     EIMVIRECSHPNIIAYFGSYIRRDRLWIVMEYCGGGSLQDIYHL-TGPLSELQIAFVCRE 118
                                                                                                                                AELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMAIRVFAKTMNNDAENKRKQA 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LREQL---SGYKRMRRQH-QKQLLALESRLRGEREEHSGRLQR-----ELEAQRAGF 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEEEGPESREMAMMQEGEHTV----TSHSSIIHRLPGSDNLYDDPYQPEMTPGPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----DEEIPTNGPKAPAESSGTVRVAKDERGQGTSGTSFQVKTVRNAGWDFSIGGSQGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKKILFQEAP-NGPGAEAPE-----EEEEAEPY----
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                                                      EVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHG 134
                                                                                             ADVIKRSNPADDYELLQRVGSGTYGEVYKARDIRSDSLAAVKVVKL---EAGDNFAVIQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E-----ELQENPSTPKREKA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGDDSK-----GTIGHRVSRSLVKMEREKP----GSSEAFIAKLIEQLGSTKEVSVKEVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RREQATDNSDYLRNSRDHSDKQRPVMRSQQVSDDEEDDSKLASLSASLSLLLLLPSLKEAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GQNDDSGSPRTPRSRLGLQERSSSASEDSISNLAEAKLALEAGFRRGNARERLGNGKYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---QPPAAPPTSTSSSSARRRAYCRNRDHFATIRTASLV-----SRQIQEHEQDSA 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEDD------SSGSGTVVIRSPRSSQSSSMFRDQSSGSTRYTSFDDASTSGTVVVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTVRALKPPQARERRQEVNSNQTSQKTSRTSGSQLSSTFGVPEISEGGFNKRDSYQNDYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTLTSLE------SSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEE
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                                                                                                                                                                         Conservative
                                                                                                                                                                                         11.0%; Score 566.5; DB 2 30.9%; Pred. No. 1.9e-10;
                                                                                                                                                                       ; 68
                                                                                                                                                                       Mismatches 185;
                                                                                                                                                                                                           DB 2;
                                                                                                                                                                     Indels
                                                                                                                                                                                                           Length
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A; Residues: 1-653 <BRA>
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A; Introns: 26/3; 101/3;
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                                                                                                                                                                                                                                                                                                                                                                             Match 11.0%; Score 565; DB 2; Local Similarity 42.3%; Pred. No. 1.7e-10; les 120; Conservative 53; Mismatches 99
                                                                                                                                                                                                                                                                                                      27
                                                                                                                                                                                                                                                                                                                                         21
EFVEMCLNKDPENRPSASTLLKHQFIKRAKKNSILVDLIERAAE 303
                                     NFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKD 299
                                                                            --KQSSYDYKADIWSLGITAIELANGEPPHSDLHPMRVLFLIPKNPPPVLQGSQWSKPFK
                                                                                                                                                    EYLHSERKIHRDIKAANVLVSEHGDVKVADFGVAGQLTETVKKRITFVGSPFWMAPELI-
                                                                                                                                                                       AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                                                    KLDPEVIFTKQERIGRGSFGEVYKGIDNRTGRVVAIKIIDL--EQAEDEIEDIQQEIQVL
                                                                                                                                                                                                                                                                                                                                       KDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFL
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                                                                                                               AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFR
                                                                                                                                                                                                                              SQCDSQYVTKYFGSFLKGSKLWIIMEYLGGGSALDLTKSGK--LDESHIAVILREILKGL
                                                                                                                                                                                                                                                               QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
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hypothetical protein T19A5.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t
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                                                                                                                                                                                                                                                                                                                                                                                  GDALLH--CGNGVIHDD------DETLRAPRAPPRTL--RAAQKAAAGNSKNRFSSTSI 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRLDARCLEQLSSSPNTSSESDRRTPTATPRSLNRGYHSERTLPAKEMPLLPD----VVG
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   29-Oct-1999 #text_change 29-Oct-1999
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submitted to the EMBL Data Library, March 1996 A; Description: The sequence of C. elegans cosmid T19A5 A; Reference number: 221512 GB/EMBL/DDBJ

Length 653; Indels

12;

Gaps

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84 80

255

201

259

142

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protein kinase (EC 2.7.1.37) BL44 - human
N;Alternate names: GC kinase
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-
C;Accession: A53714
R;Katz, P:, Whalen, G.; Kehrl, J.H.
J. Biol. Chem. 269, 16802-16809, 1994
A;Title: Differential expression of a novel pr
A;Reference number: A53714; MUID:94266900; PMI
A;Accession: A53714
• submitted to the EMBL Data Library, A; Reference number: Z19041
A; Accession: T18897
A; Status: preliminary; translated fa, Molecule type: DNA
A; Residues: 1-1228 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status; preliminary
A;Status; preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-819 <KATP-
A;Cross-references: GB:U07349; NID:g531819; PIDN:AAA20968.1; PID:g531820
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
C;Keywords: ATP; phosphotransferase
F;13-272/Domain: protein kinase homology <KIN>
F;21-29/Region: protein kinase ATP-binding motif
                                                                                                         hypothetical protein C04A11.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T18897 R;McMurray, A.
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                                                                                                                                                                                                                                                                              -TIKRAPFLGPLPTDPPAEEPLSSPPGTLPPPPSGPNSS
                                                                                                                                                                                                                                                                                                                                                   -ELSGSLLQSVQEALEERSLTIRSASEFQELDSPDDTMG
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31.7%; Pre
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Pred. No. 2.6
                                                                                          November
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Mismatches 176;
                                    GB/EMBL/DDBJ
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A;Map position: X
A;Introns: 25/3; 107/3;
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                                               EQARKFTSEQTNLTRTSELEMDAMERRQRKE1EDTEGAQEHELRNAQKRLR1EQEKDMRA
                                                                                                                                                                         DYEGNAKENAAPSPVPVPKISOKPVPTPS-TSTDVQKTNSNVAPR-PLGGRKDGNRQTIT
                                                                                                                                                                                                                                      PKRAESNQSYRTSGSSNSVVQHSASSSTDYYPTSYSAVPEYFDGPRRNGEQKVPPPEPPV
                                                                                                                                                                                                                                                                                                  IVAQKKVSREEAEAVQHSNALFKKPSQDMSASLTVRDMAQQKTELRVSSASTPTKTRASP
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                                                                                                             KKTRTYMIDGVQVTSTTVHVLGVKDDKVQRKQQLHDLRRLQRDEARQKQELQAEGIKLVE
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                                                                                                                                                                                                                                                                       --TSTSSSSARRRAYCRNRDHFAT
                                                                                                                                                                                                                                                                                                                                 EHTVTSHSSIIHRLPGSD-----NLYDDPYQP-----EMTPGPLQPPAAP
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                                                                                                                                                                                                                                                                                                                                                                                                - VNSLADASDNEEEEEEEEEEEEEEEEGPESREMAMMQEG
                                                                                                                                                                                                         ----IRTASLVSRQIQEHEQDSALREQLSGYKRMRRQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AGT----
                                                                            RHQAIGEKEARAAQAEE-RKFQQHILGQQKKELAA
                                                                                                                                            ----HQKQLLALESRLRGEREEHSGRLQRE----LE
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,	рb	Qy	Ър	Qy	Db	Qy	рь	Qy	Db	Qy	Db
•	1176	869	1132	810	1089	750	1038	694	982	636	923
	1176KYHEMRELWQENLIARKTVLEEKFEDE 1202	TPVPE	1132 KSQKKLQILKERHQEAIIELDEMQNEKRKQLLEKERNTMKEHEA- 1175	EMGTFSSSPQKHRSLVNEEDWDISKEMKESRVPSL	1089 VMFKESLRISAVNMSNAEMQERIRRFDEQEALRMRAALEDHDL 1131	750 GQLPMGLPATGALGPLSTGTLSEEQPCSSGQEAILGQRMLGEEEEAVPERMILGKEGTTL 809	1038 LLRTQMLARHQREMAQIEKIHQEEEDDLIRALTLDRKKLPKMLRSETKTRS 1088	LRQLQAVQRTRAELTRLQHQTELGNQLEYNKRREQELRQKHAAQVRQQPKSLKVRA 749	RMAEKHKERMASIEKQFLMQKHNLLRAKENNIWELEDKOMREKFVLHRKLFKDEYY 1037	RQRQYFELQCRQYKRKMLLARHSLDQDLLREDLNKKQTQKDLECALLLRQHEATRELE 693	923 FKERLKQEMKIFKQELTMLSKYQRKDALKQRKEQIEIEHQLKEKDFLMQLQQNAEA-MLQ 981

Search completed: November 22, 2002, 12:27:14 Job time : 36.804 secs

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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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        ion update)
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

-I FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYBLIN BASIC PROTEIN HISTONE IIA ON SERINE AND THREONINE RESIDUES (BY SIMILARITY).

-I CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-I TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGAN.

-I PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                Prodom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS00118; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed: Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oriented kinase, and comparative mouse, and rat homologues."; Immunogenetics 49:369-375(1999).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; pkinase;
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InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB015718; BAA35073.1; -. EMBL; AL133081; CAB61400.1; -. HSSP; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bloecker
                                                                                                                                                                                                                                                         Phosphorylation;
                                                                                                                                                                                                                                                                        Transterase;
                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                        MIM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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CDHPYIVKLLGAYYHDGKLWIMIEFCPGGAVDAIMLEL-DRGLTEPQIQVVCRQMLEALN
                         LRHPNTIQYRGCYLREHTAWLVMEYCLGSASD - - LLEVHKKPLQEVEIAAVTHGALQGLA
                                                                             DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
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                                                                                                         Conservative
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                                                                                                                                                                                                                                                                   Serine/threonine-protein kinase;
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                                                                                                                                                              AA;
                                                                                                                                                                                                                                                          Coiled
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COILED COIL (POTENTIAL).
GLN-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                        Score 695; DB 1;
Pred. No. 1.8e-21;
4; Mismatches 366
                                                                                                                                                                            ВҮ
                                                    KNKETGALAAKVIETKSEEELEDYIVEIEILAT
                                                                                                                                                              15E245193ECC553D CRC64;
                                                                                                                                                                           SIMILARITY
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E
                                                                                                                                 Length 968,
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RESULT 3
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ID ST10_MOUSE
AC 055098;
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DT 16-0CT-2001
DT 16-0CT-2001
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16-0CT-2001
16-0CT-2001
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Serine/threonine-protein kinase 10 (EC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEY
                                                                                                                                                                                          IGTPRDPGDGCPSPDIP 929
                                                                                                                                                                                                                       HLLVEHETQKLKALDESHNQNLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEA---
                                                                                                                                                                                                                                                    NIIGQEEAGAWNLWEKEHG-NLVDMEFKLGWVQGPVLTPVPEEEEEEE-----
                                                                                                                                                                                                                                                                                                                MILGKEGTTLEPEEQRILQEEMGTFSSSPQKHRSLVNEEDWDISKEMKESRVPSLASQER
                                                                                                                                                                                                                                                                                                                                              IQRSEGKTRMAMYKKSLHINGG-----GSAAEQ-----REKI---KQFSQQEEK----
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                                                                                                                                                           ECPNPSTP
                                                                               STANDARD;
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                                                                               PRT;
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ion update) (EC 2.7.1.
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Best Local Similarity
Matches 245; Conserv
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                                                                                                                                                                                                                                                                                                     NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D89728; BAA24073.1; -. HSSP; P24941; 1CKP. MGD; MGI:1099439; Stk10. InterPro; IPR000719; Euk_Pkinase. InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predominantly in lymphocytes.";
J. Biol. Chem. 272:22679-22684(1997).
-i- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYBLIN BASIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PTM: AUTOPHOSPHORYLATED.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HISTONE IIA ON SERINE AND THREONINE RESIDUES.
-i- CATALITIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-i- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLX IN LYMPHOID ORGANS
SUCH AS SPLEEN, THYMUS, AND BONE MARROW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuramochi S., Moriguchi
Karasuyama H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase).
STK10 OR LOK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97426413; PubMed=9278426;
Kuramochi S., Moriguchi T., Kuida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "LOK is a novel mouse STE20-like protein kinase that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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207
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                                                                                                                      CDHPYIVKLLGAYYYDGKLWIMIEFCPGGAVDAIMLEL-DRGLTEPQIQVVCRQMLEALN 146
                                                                                                                                                                                  DPNDVWEIVGELGDGAFGKVYKA---KNKETGALAAAKVIETKSEEELEDYIVEIEILAT
ETMKDAPYDYKADIWSLGITLIEMAQIEPPHHELNPMRVLLKIAKSDPPTLLTPSKWSVE
                 -AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEY
                                                                           YLHSHNMIHRDVKAGNILLSEPGLVKLGDFG----SASIMAPANSFVGTPYWMAPEVIL- 195
                                                                                                                                                  LRHPNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKPLQEVEIAAVTHGALQGLA 140
                                                           FLHGKRIIHRDLKAGNVLMTLEGDIRLADFGVSAKNLKTLQKRDSFIGTPYWMAPEVVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        0011; PROTEIN_KINASE_DOM; 1.
Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Coiled
                                                                                                                                                                                                                                                                                                                    294
936
883
50
65
157
                                                                                                                                                                                                                                                                                                        111992
                                                                                                                                                                                                                                                          13.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                coil
                                                                                                                                                                                                                                            174;
                                                                                                                                                                                                                                                                                                        WW.
                                                                                                                                                                                                                                                                                                                    GLN-RICH.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                         Score 692.5; DB 1;
Pred. No. 2.3e-21;
'4; Mismatches 347;
                                                                                                                                                                                                                                                                                                                                                                               COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE
                                                                                                                                                                                                                                                                                                 SIMILARITY.
7115EAC01032BF94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Κ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endo J.,
                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Semba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration -
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                            253
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RESULT 4
STK4_H
ID STK4_H
ID STK4_H
AC Q13043
DT 16-OCT
DT 16-OCT
DT 16-OCT
DT (Serine
DE MST1)
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                                                                                                                                                         STR4_HUMAN STANDARD; PRT; 487 AA. Q13043; Q15802; Q9NTZ4; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Serine/threonine protein kinase 4 (EC 2.7.1.37) (STE20-like MST1) (MST-1) (Mammalian STE20-like protein kinase 1) (Serine/threonine protein kinase Krs-2).
MEDLINE-95394929; PubMed-7665586; Creasy C.L., Chernoff J.; "Cloning and characterization of
                                                                                                      STK4 OR MST1.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                    SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                             894
                                                                                                                                                                                                                                                                                                                                                                                                            839
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                                                                                                                                                                                                                                                                                                                                                                                                         DWDISKEMKESRVPSLASQERNIIGQEEAGAWNLWEKEHGNLVDMEFKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QQQEKARLPKIQRSDGETRMAMYKKSLHINGA-----GSASE-----QREKIKQFSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QPQEPVNGPCSQPSGDGPLQTTSPADGLSKNDNDLKVPVPLRKSRPLSMDARIQMDEEKQ
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     þ
   human
 protein
                                                                                                      Hominidae;
   kinase with homology
                                                                                                                    Euteleostomi;
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Matches 169
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                                                                                                                                                                                                                                                                                                                                                 PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P24941; 1HCL.
Genew; HGNC:11408; STK4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U18297; AAA83254.1; -. EMBL; U60207; AAB17262.1; -. EMBL; AL109839; CAB89421.1; -HSSP; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
-!- PTM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taylor L.K., Wang "Newly identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-96413604;
                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                     Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to Ste20.";
J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000719; Euk_pkinase
  179
                          121
                                                                             64
                                                                                                     64
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                                                                                                                                                      LKDPDVAELFFKDD-----PEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSG
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ANSFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIA
                          LTEDEIATILQSTLKGLEYLHFMRKIHRDIKAGNILLNTEGHAKLADFGVAGQLTDTMAK 180
                                        LQEVETAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAP 178
                                                                                                                             LRNPPRRQLKKLDEDSLTKQPEEVFDVLEKLGEGSYGSVYKAIHKETGQIVAIKQVPV--
                                                                          ---ESDLQEIIKEISIMQQCDSPHVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKT 120
                                                                                                    KQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>۾</u>
                                                                                                                                                                                                                                                                                                                                               PS00107; PROTEIN_KINASE_ATP; 1.
PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002290; Ser_thr_pkinase
IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                  487
                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                    Serine/threonine-protein kinase; ATP-binding
                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                           pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270:21695-21700(1995).
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H.C., Erikson R.L.;
stress-responsive p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci. U.S.A. 93:10099-10104(1996)
                                                                                                                                                                                                                                              44
59
149
378
222
312
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                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                 ;88
                                                                                                                                                                                                                                                                     PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-GLU.
                                                                                                                                                                              Score 619; DB 1; Length 487; Pred. No. le-18; Mismatches 191; Indels 1
                                                                                                                                                                                                                                P -> R (IN REF. 1).
V -> M (IN REF. 1).
; 150758EBC5F77D5C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                Indels 124;
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MRL outstation -
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                                                                                                                                                                                Gaps
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RESULTION OF THE RESULT OF THE RESULTION OF THE RESULT OF THE RESULTION OF THE RESULT OF THE R
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STK3_HUMAN STANDAKL;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 3 (EC 2.7.1.37) (STMST2) (MST-2) (Mammalian STE20-like protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and characterization of a Ste20-like kinases."; Gene 167:303-306(1995).
                                                                                                                                                                                            MEDLINE=94100173; PubMed=8274451;
Schultz S.J., Nigg E.A.;
"Identification of 21 novel human protein kinases, including
of a family related to the cell cycle regulator nimA of Asper
                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96413604;
Taylor L.K., Wang
"Newly identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Creasy C.L.,
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Eukaryota; Metazoa; Chordata;
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MEDLINE=96144292; PubMed=8566796;
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CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein SUBCELLULAR LOCATION: Cytoplasmic (By similarity). TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT KIDNEY, SKELETAL AND PLACENTA TISSUES AND AT VERY LOW LEVELS IN ADULT HEART, LUNG AND BRAIN TISSUES.
                                                                                                                  l Growth Differ. 4:821-830(1993).
FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
                                                                                                   SIMILARITY)
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H.C., Erikson R.L.;
stress-responsive p
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Query Match
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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IPR002290;
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ATP (BY SIMILARITY)
BY SIMILARITY.
POLY-GLU.
POLY-GLU.
WIV -> YLY (IN REF. 3)
D -> Y (IN REF. 3)
D -> E (IN REF. 2).
GEC -> ESY (IN REF. 2).
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No. 7.2e-18;
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                                             409
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410

CNQNMHEPFPMSKNVFPDNWK

430

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                                           Вb
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                                                                                                                                                             Query Match
Best Local
                                                                                                    Matches
                                                                                                                                                                      Phosphorylation.
DOMAIN 20
NP_BIND 26
BINDING 49
ACT_SITE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Z2W1;
16-OCT-2001
                                                                                                                                                                                                                                          PROSITE; PS00108; PROTEIN_KINASE_ST; F
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
Transferase; Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic mapping of human and mouse PAK genes.";
Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
-i- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE
-MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant stress response kinase 1) (Ste20/oxidant stress response kinase-1)
(SOK-1) (Ste20-like kinase).
                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                      Pfam, PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1891699; Stk25.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF004934; AAD01208.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Melnick M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STK25 OR SOK1.
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                83
                                             15
                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS THE KINASE ACTIVITY (BY SIMILARITY). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ATP + a protein = ADP +
            LRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY
                                     DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVALKIIDL--EEAEDEIEDIQQEITVLSQ 72
                                                                DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _MOUSE
                                                                                                                Similarity
                                                                                                                                                             126
                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                        PROTEIN_KINASE_ST; FALSE_NEG
                                                                                                                                                                         270
34
49
140
                                                                                                               11.6%;
                                                                                                                                                            48175
-:
-:
-:
                                                                                                                                                            MW;
                                                                                          Score 597.5; Db ., Pred. No. 6.5e-18;
                                                                                                   68;
                                                                                                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Sciurognathi; Muridae;
                                                                                                                                                          6A01916034E26362 CRC64;
426
                                                                                                                                                                                                                                                kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLY
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                                                                                                 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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RESULT 7
ST24_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q916ED; O14840;
Q916ED; O14840;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 24 (EC 2.7.1.37) (S
                                                                                                                                                                                                                                                                                                                                   Schinkmann K., Blenis J.; "Cloning and characterization of a human with unusual cofactor requirements."; J. Biol. Chem. 272:28695-28703(1997).
                                                                                       -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoproteir
-!- COFACTOR: ISOFORM A REQUIRES MANGANESE FOR ITS ACTIVITY.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: ISOFORM A IS UBIQUITOUS. ISOFORM B IS
                                                                                                                                                                                                   J. Biol. Chem.
                                                                                                                                                                                                                              STE20-like kinase
                                                                                                                                                                                                                                                                      Zhou
                                                                                                                                                                                                                                                                                   MEDLINE=20112812;
                                                                                                                                                                                                                                                                                                 TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MST3) (MST-3) (Mammalia
STK24 OR MST3 OR STK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ST24_HUMAN
                                                                                                                                                                                      -!- FUNCTION:
                                                                                                                                                                                                                 kinase."
                                                                                                                                                                                                                                          "Identification of a
                                                                                                                                                                                                                                                        Pei G
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98019249;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       404
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         PTM: AUTOPHOSPHO
BY PKA.
SIMILARITY: BELO
STE20 SUBFAMILY.
                                                               EXPRESSED IN BRAIN WITH CEREBRAL CORTEX.
                                                                                                                                                                           RESIDUES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF
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                                                  AUTOPHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGHGEESSSEDSDIDGEAEDGEQGPIWTFPPTIRPSPHSKLHKG---TALHSSQK
                                                                                                                                                                                      PROTEIN
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PROTEIN KINASE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                       BELONGS
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PubMed=9353338;
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                                                                                                                                                                                                                                                                                                           (ISOFORM B), AND MUTAGENESIS
                                                                                                                                                                                                                           that is regulated
                                                                                                                                                                                                                                            human
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                       TO
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s regulated by o
                       THE SER/THR
                                                                           HIGH EXPRESSION
                                                 ISOFORM
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                       FAMILY OF
                                                 \mathbf{SI}
                                                                                                                                                                                                                           cAMP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                      BOTH
                                                                                                                                                                                                                                                                                                                                                                  STE20-like
                                                                                                                                                         ADP + a phosphoprotein
                                                                                                                                                                                                                                          isoform of mammalian
                                                 ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
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                                                                           IN HIPPOCAMPUS
                                                                                                                                                                                     SERINE AND THREONINE
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                       PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (STE20-like kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
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                                                 PHOSPHORYLATION
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a collaboration

no 9

way

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RESULT 8
ST25_HUMAN
ID ST25_H
AC 000506
DT 16-OCT
DT 16-OCT
DT 16-OCT
DE Serine
DE Stress
DE (SOXT)
GN STR25_1
GN STR25_
OS HOMO S
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Best Local S
Matches 130
           000506; Q15522;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant stress response kinase 1) (SCC-1) (SCC-1) (Ste20-like kinase).
STK25 OR SOKI OR YSKI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00109; TYRKINASE.

Prodom; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKc; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.

      Phosphorylation;
      Alternative splicing.

      DOMAIN
      36
      286
      PROTEIN KINASE.

      NP_BIND
      42
      50
      ATP (BY SIMILAR BINDING
      65
      ATP (BY SIMILAR BINDING

      ACT_SITE
      156
      BY SIMILARITY.
      BY SIMILARITY.

      MOD_RES
      18
      PHOSPHORYLATION

      VARSPLIC
      1
      26
      MDSRAQLWGLAINKR

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                                                                                                                                                                                                                                                                                                                                                                                                                                    256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; AF083420;
; P24941; 10
                                                                                                                                                                                                                                                                                                                                                                                                           NFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPT-VIMDLIQRTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE-GNYSKPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        604984; -
                                                                                                                                                                                                                                                                                                                                                                             EFVEACLNKEPSFRPTAKELLKHKFILRNAKKTSYLTELIDRYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGNC:11403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414
443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAD42039.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49307 MW;
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45.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GMO (IN ISOFORM A).
T->A: LOSS OF PHOSPHORYLATION
A -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 594; DB 1;
Pred. No. 9.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY PKA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4A9FF1F6B6A88A97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                            426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                               298
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and SPS1, but is not involved in the known MAPK pathways.";
Oncogene 14:2047-2057(1997).
-!- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE
MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohno S
"YSK1,
                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre Luropean Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=97304522; PubMed=9160885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=97042345; PubMed=8887545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               novel stress response pathway.";
EMBO J. 15:4537-4546(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pombo C.M., Bonventre J.V., Molnar A., Ky "Activation of a human Ste20-like kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Osada
                                                                                                                                                                                                                                                                                                                                                                                                        HEART AND LUNG. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                              STE20 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THE KINASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a novel mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mizuno K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kyriakis J., Force T.;
se by oxidant stress defines
                                                                                                                                                                                                                                                                                                                            There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki A.,
                                                                                                                                                                                                                                                                                                                  Usage
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STOMACH
                                                                                                                                                                                                                                                                                                                  bу
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                                                                                                                                                                                                                                                                                                                   and for
                                                                                                                                                                                                                                                                                                                                                     EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                  a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to Ste20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARE
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Ş Matches Query Match Best Local ACT\_SITE PROSITE; PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.
PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1. Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk\_pkinase;
SMART; SM00220; S\_TKC; 1. EMBL; X99325; CAA67700.1; EMBL; D63780; BAA20420.1; HSSP; P12931; 1FMK. SEQUENCE InterPro; IPR000719; Euk\_pkinase.
InterPro; IPR002290; Ser\_thr\_pkinase MIM; Genew; 23 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 602255; 154; HGNC:11404; STK25 Similarity 426 Conservative Serine/threonine-protein kinase; ATP-binding; AA; 270 34 49 48111 MW; 11.5%; 68; Pred. ΕP ATP (BY SIMILARITY).
ATP (BY SIMILARITY). Score 183CE5700FCEA716 CRC64; Mismatches SIMILARITY. 591; No. 1 DB 1; .2e-17; 129; Length 426; Indels 72; Gaps 82

δÃ 밁

83 73

LRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141 CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY

DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ

72

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P35465; Q62934;

Q1-JUN-1994 (Rel. 29, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated)

Serine/threonine-protein kinase PAK (Protein kinase MUK2).
                                                                                                                                                            [4]
TISSUE SPECIFICITY.
MEDLINE-96027610; PubMed-7559638;
Medline-96027610; Thao Z.-S.,
                                                                                                                                                                                                                                                                                              Zhao
                                                                                                       "Molecular cloning of a new member of
kinase (PAK) family.";
J. Biol. Chem. 270:25070-25078(1995).
-i- FUNCTION: THE ACTIVATED KINASE ACT
                                                                                                                                                                                                                                  Osada S.-I.,
Ohno S.;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     Submitted
                                                                                                                                                                                                                                                                                                                        Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                          -
                                                                   ---
                                                                                                                                                           111
                                                                                                                                                                                                                     Submitted (JUL-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                              REVISIONS
                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94150588; PubMed=8107774;
Manser E., Leung T., Salihuddin H.
"A brain serine/threonine protein
                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
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BIOL: Chém. 270:25070-25078(1995).

FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TLIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-F GTPASES TO THE JNK MAP KINASE PATHWAY.

SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDE CDC42/P21 AND RAC1 (BY SIMILARITY).

TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BR HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.

DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH
                                                                                                                                                                                                                                                                                               2.-S
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                                                                                                                                                                                                                                                                                                                                    367:40-46(1994)
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                                                                                                                                                                                                                                              Izawa
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                                                                                                                                                                                                                                            Saito R., Mizuno K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                            H., Zhao
in kinase
                                                                                                                                                                   Leung
                                                                                                                                           the
                                                                                                                                                                   T:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata;
                                                                                                                                                                                                                                                                                                                                                           Z.-S., Lim
activated k
                                                                                                                                          p21-Cdc42/Rac-activated
                                                                                                                                                                   Michael
                                                                                                                                                                                                                                           Suzuki A., Hirai S.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEEEE----
                                                                                                                                                                                                                     databases
                                        IN THE BRAIN,
                                                                 NOT GDP-BOUND
                                                                                                                                                                                                                                                                                                                                                        n L.
                                                                                                                                                                   G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
                                                                                         RHO-RELATED
                                                                                                     OF TARGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                Murinae;
                                                                                                                                                                                                                                                                                                                                                           Cdc42
                                                                                                                                                                   Hall
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                            MOTOR
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                                                                                                                                                                   С.,
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                                        HTIW
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BARAR

PAK1\_HUMAN STAN Q13153; Q13567; Q1-NOV-1997 (Rel. 3 01-NOV-1997 (Rel. 3 15-JUN-2002 (Rel. 4

STANDARD;

PRT;

545

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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-)

(p21-activated

35, 35,

Created)

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RESULT 10
PAK1_HUMAN
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                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                                          Phosphorylation.
DOMAIN 75
DOMAIN 134
DOMAIN 269
NP_BIND 275
BINDING 298
                                                                                                                                                                                                                                                                                                                                              DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50108; CRIB; 1.
PROSITE; PS50107; PROTEIN_KINASE_ATP; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P24941; 1CKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; S40482; S40482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U23443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY SIMILARITY: BELONGS TO THE SER/THR FAMILY STE20 SUBFAMILY.
SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXPRESSION ELSEWHERE
                                                                     FYDSCLQKIPQDRPTSEVLLKHRFYLRERPPTVIMDLIQRTKDAVR 302
                                                                                                                                                          LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                        DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                    DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collal een the Swiss Institute of Bioinformatics and the EMBL outs European Bioinformatics Institute. There are no restrictions
                                             FLNRCLEMDVEKRGSAKELLQHQFLKIAKPLSSLTPLIAAAKEATK
                                                                                                                    DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN
                                                                                                                                         NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALEF
                                                                                             TRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRD
                                                                                                                                                                                                                                                                                      il Similarity
117; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U49953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD000001;
                                                                                                                                                                                                                                                                                                                                     544
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB95646.1;
AAB61533.1;
                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                268
520
520
283
298
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                                                                                                                                                                                                                                                                                      52;
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PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                  Pred. No. 2.8e
2; Mismatches
                                                                                                                                                                                                                                                                                                 Score 510;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                         CRIB.
                                                                                                                                                                                                                                                                                                                                     93BE32D8222F5B7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         --
                                                                                                                                                                                                                                                                                                DB 1;
.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as
                                                                                                                                                                                                                                                                                       103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y CDC42/P21.
Y OF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    its content
                                                                                                                                                                                                                                                                                                           Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINASES
                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in no way commercial
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                            435
                                                                                                                                                                   197
                                                                                                                                                                                          378
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Query Match
                                 CONFLICT
                                                                             DOMAIN
NP_BIND
BINDING
ACT_SITE
MUTAGEN
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[2]
                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This
                        SEQUENCE
                                                                                                                                                                                                                        ProDom; PD000001; Euk_pki
SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-97199447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00095; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                          EMBL; U51120;
HSSP; P24941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Placenta;
MEDLINE-96398842; PubMed-8805275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sells M.A., Knaus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase 1)
                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase; 1.
Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brown J.L., Stowers L., Baer M., Trejo J., "Human Ste20 homologue hPAK1 links GTPases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                     DOMAIN
                                                                                                                                                           Phosphorylation
                                                                                                                                                                      Pransferase;
                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Human p21-activated kinase (Pak1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-GTPASES TO THE JIK MAP KINASE PATHWAY.
SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GE CDC42/P21 AND RAC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 CRIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY SIMILARITY: BELONGS TO THE SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STE20 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                      602590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. 7:202-210(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biol. 6:598-605(1996).
                                                                                                                                                                                                                                                                                                                             HGNC:8590; PAK1.
                                                                                                                                                                                PS00108;
                                                                                                                                                                                           PS50011;
                                                                                                                                                                                                    PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                 PS50108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PAK-1)
                                    75
134
270
276
299
299
389
107
107
26
237
379
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                                                                                                                                                                     Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                           1CKP
                                                                                                                                                                                                                                                                                                                                                               AAA65441.1; -.
                                                                                                                                                                                                                                                                                                                                                     AAC50590.1;
                                                                                                                                                                             PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9395435;
U.G., Bagrodia S.,
                                                                                                                                                                                                                                               Euk_pkinase;
                                                                                                                                                                                                                  CRIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (P65-PAK) (Alpha-PAK)
                                              88
269
521
284
299
299
389
107
107
237
                         60661
  .98;
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                                                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                L->F: CONSTITUTIVELY ACTIVE.
V -> A (IN REF. 2).
R -> L (IN REF. 2).
F -> S (IN REF. 2).
D -> E (IN REF. 2).
  Score 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                     LINKER
                       14A1E70E6480CD7E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulates
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  DB
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OF PROTEII
                                                                                                                                                                   ATP-binding;
                       CRC64;
Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHO-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TARGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
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RESULT 11
PAK1_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAK1_MOUSE 
088643;
                                                                                                                                                                                                 This SWI
between
                      EMBL; AF082077; AAC32375.1; -.
HSSP; P24941; 1CKP.
MGD; MGI:1339975; Pak1.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00095; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                          the European Bioinformatics Institute. There are no use by non-profit institutions as long as its con modified and this statement is not removed. Usage by entitles requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99282526; PubMed=10352232; Burbelo P.D., Kozak C.A., Finegold A.A., Hall merous system expression and the mouse PAK-1 and PAK-3 genes."; Gene 232:209-215(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAK-A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAK1 OR PAKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinase 1) (PAK-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497
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                                                                                                                                                                                                                                                                                                  FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.

LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED GTPASES TO THE JNK MAP KINASE PATHWAY (BY SIMILARITY).

SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RAC1 (BY SIMILARITY).

PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21 (BY
                                                                                                                                                                                                                                           STE20 SUBFAMILY.
SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                                                                        SIMILARITY).
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLNRCLDMDVEKRGSAKELLQHQFLKIAKPLSSLTPLIAAAKEATK 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV---VTETCMDEGQIAAVCRECLQALEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s (Mouse).
s (Mouse).
Metazoa; Chordata; C:
Metazoa; Rodentia; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                         BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         νιυτειή Kinase PAK 1 (EC 2.7́.1.-)
(P65-PAK) (Alpha-PAK) (CDC42/RAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.98;
                                                                                                                                                                                                                                                                        THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vert Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                         SER/THR
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                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                         FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ā
                                                                                                                                                                    as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104;
                                                                                                                                                                                                                                                                                                                                                                                                                      ll A., Pirone D.M.;
and chromosomal mapping
                                                                                                                                                                                                                                                                         OF.
                                                                                                                                                                                                                                                                         PROTEIN KINASES
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                                                                                                                                                        Λq
                                                                                                                                                                                   restrictions
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PF00069;

pkinase; PBD; 1.

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PAK3
      A TOUR PROPERTY OF THE PROPERT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q62829;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
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PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
      <del>-</del>
                                                                                                                                                                               kinase (PAK) family
J. Biol. Chem. 270:
                                                                                                                                                                                                                                                       WIT
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                <del>-</del>
                                                                                                                                                                                                                                                                                                 MEDLINE=96027610;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00107; PROTEIN_KINASE_ATP; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                           "Molecular cloning of a new member of the p21-Cdc42/Rac-activated
                                                                                                                                                                                                                                                                       Manser E., Chong C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAK3_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation. 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase;
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                                                                                       Biol. Chem. 270:25070-25078(1995).

FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.

SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RACI. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3

DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK
                                              SIMILARITY).
TISSUE SPECIFICITY:
LOW LEVELS IN THE TE DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLQCCLEMDVEKRGSAKELLQHQFLKIAKPLSSLTPLMHAAKEATK 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV---VTETCMDEGQIAAVCRECLQALEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPKKKYTPFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV----
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116; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00285; PBD;
SM00220; S_TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PD000001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S_TKC; 1
                                                                                                                                                                                                                                                                                            PubMed=7559638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRIB;
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                                                                                                                                                                                                                                                                       Zhao
                       TESTIS
                                           DETECTED AT HIGH LEVELS
                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE OF
    FOUND
                                                                                                                                                                                                                                                                     Z.-S., Leung T., Michael G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 508; DB 1;
Pred. No. 3.3e-14;
2; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LINKER
    IN
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  THE
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EMBRYONIC
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                                              Z
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                                              THE
                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                         Murinae;
                                              BRAIN AND
                                                                                                                                                                                                                                                                     Hall C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
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                                                                                       (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                  RESULT 13
PAK3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 116
         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-)
kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3).
                                                                                     PAK3_HUMAN
075914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRODOM; PD000001; Euk_pkinase; 1.
SMART; SM00225; PBD; 1.
SMART; SM00220; S.TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS500107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00108; PROTEIN_KINASE_ST; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial contents are the statement in the statement in the statement is not removed. Usage by and for commercial contents are the statement in the statement in the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation. DOMAIN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U33314; AAC52268.1; -. HSSP; P24941; 1CKP. InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                             495
                                                                                                                                                                                                                                                                                                                                                       320
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                                                                                                                                                                                                                                                               198
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                                                                                                                                                                                                                                                                                                                                                                                                                                             23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
mes 116; Conserv
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PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED SIMILARITY: BELONGS TO THE SER/THR FAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STE20 SUBFAMILY
OR OPHN3
                                                                                                                                                                                                     FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR
                                                                                                                                                                                                                                                                                            LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV----
                                                                                                                                                                                                                                                                                                                                                    LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY
                                                                                                                                                                           FINRCLEMDVDRRGSAKELLQHPFLKLAKPLSSLTPLILAAKEAIK
                                                                                                                                                                                                                                                   DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEYFRN
                                                                                                                                                                                                                                                                                                                         LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                          DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
                                                                                                                                                                                                                                  TRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQNPERLSAVFRD
                                                                                                                                                                                                                                                                                                                                                                                                                DPKKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNL---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein
                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAKbox/Rhobndng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LINKER.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 505; DB 1;
Pred. No. 4.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7B940FC204A2B48B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 104;
                                                                                                  544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                              -QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                           (p21-activated
                                                                                                                                                                           540
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                                                                                                                                                                                                                                                                                                                         197
                                                                                                                                                                                                                                                                                                                                                                                 141
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                                                                                                                                                                                                                                     494
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Best Local S
Matches 116
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BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allen K.M., Gleeson J.G., Bagrodia S., Partington M.W., Macmillan J.C., Cerione R.A., Mulley J.C., Walsh C.A.; "PAK3 mutation in nonsyndromic X-linked mental retardation."; Nat. Genet. 20:25-30(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00095; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF068864; AAC36097.1; HSSP; P24941; 1CKP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98400251; PubMed=9731525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SH3-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew;
                                               142
                                                                                                                                                                                                    263
                                                                                                                                                    83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUTN NOT GDP-BOUND
CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN POSTMITOTIC NEURONS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPING AND POSTNATAL CEREBRAL CORTEX AND HIPPOCAMPUS. PYM: AUTOPHOSPHORYLLATED WHEN ACTIVATED BY CDC42/P21. DISEASE: DEFECTS IN PAK3 ARE A CAUSE OF AN X-LINKED FORM OF NONSYNDROMIC MENTAL RETARDATION (MRX30).

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens (Human).
Motazoa; Chordata;
                                                                                                                                                                                                                                    DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                             LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                            NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQ1AAVCRECLQALDF
                                                                                                                            DPKKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNL---QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:8592; PAK3
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50108; CRIB; 1.
PS00107; PROTEIN_KINASE_ATP; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                ; Phosphorylation.
70 83 C
70 83
129 267 L
268 519 P
274 282 A
297 A
387 387 B
544 AA; 60692 MW;
                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primates;
                                                                                                                                                                                                                                                                                                                           9.8%;
                                                                                                                                                                                                                                                                                                      52;
                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                           Score 504;
Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                        230AF6952CB049E2 CRC64;
                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                        DB 1;
1.8e-14;
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                                                                                                                                                                                                                                                                                                   104;
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                                                                                                                                                                                                                                                                                                                                                   Length 544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                               141
                                                                                            377
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RESULT 14
PAK3_MOUSI
ID PAK3
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PAK3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  061036; 088645;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated kinase 3) (BAK-3) (BEK2-PAK) (CDC42/RAC effector kinase PAK-B).
PAK3 OR PAK-3 OR STK4 OR PAKB.
                                                                                                                                                                                                                                    MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=96032693; PubMed=7559398; Bagrodia S., Taylor S.J., Creasy C.L., Carticle S.J., Creasy C.L., Carticle S.J., Creasy C.L., Carticle S.J., Carticle S.J., Creasy C.L., Carticle S.J., Carticle S.J.,
                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burbelo P.D., Kozak C.A., Finegold A.A., "Cloning, central nervous system express:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                          HSSP;
                                                                                                                                                                                                                                                                                   EMBL; AF082297;
                                                                                                                                                                                                                                                                                                      EMBL; U39738;
                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99282526; PubMed=10352232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                        MGI:1339655; Pak3.

rPro; IPR000719; Euk_pkinase.
rPro; IPR000095; PAKbox/Rhobndng.
rPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLNRCLEMDVDRRGSAKELLQHPFLKLAKPLSSLTPLIIAAKEAIK
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                                                                                                                                                                                                                                                             P24941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Taylor S.J., Creasy C.L., n. 271:1250-1250(1996).
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                                                                                                                                                                                                                                                                                   AAC31969.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chernoff J., Ceric
c activated kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chernoff J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hall
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nd chromosomal
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inase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cerione
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                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
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SMART; SM00285; PBD; 1. SMART; SM00220; S\_TKC; 1. PROSITE; PS50108; CRIB; 1

PS00107; PROTEIN\_KINASE\_ATP;

ProDom; PD000001; Euk\_pkinase;

PBD; pkinase;

Pfam; PF00069; Pfam; PF00786;

InterPro;

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RESULT 15
SPS1_YEAST
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P08458;
P08458;
O1-NUG-1988 (Rel. 08, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Sporulation-specific protein 1 (EC 2.7.1.-).
SPSI OR YDR523C OR D9719.27.
SPSI OR YDR523C OR D9719.27.
                                                                                                                                         Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Winant A., Yelton M., Botstein D., Davis R.W.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NP_BIND
BINDING
ACT_SITE
CONFLICT
expressed preferentially during sporulation
                   SEQUENCE OF 396-490 FROM N.A. MEDLINE=87064542; PubMed=3023934; Percival-Smith A., Segall J.; "Characterization and mutational analysis"
                                                                                                                                                                                                                                                                                                                                                                    Friesen H., Lunz R., Doyle S., Segall J.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Friesen H., Lunz R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPS1_YEAST
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297 297
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525 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ascomycota; Saccharomycotina; Sacch
Saccharomycetaceae; Saccharomyces
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G -> A (IN REF.
V -> E (IN REF.
H -> R (IN REF.
L -> M (IN REF.
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PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).
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> E (IN REF. 3).
> R (IN REF. 3).
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cluster of three
Saccharomyces
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                                                                                                                                                                                                                    Petel F.X.,
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Matches
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CONFLICT
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ACT_SITE
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108: PROTEIN_KINASE_ST; FALSE_NEG
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U13018; AAA64833.1; -. EMBL; U33057; AAB64963.1; -. EMBL; M13629; AAA35079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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les 135; Conserv
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SIMILARITY: BELONGS
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QTVTPITNPSS
                                                                                                                                                                                                         AGCLVKTPADRPSAYNLLSFEFV---
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                                                    MSISASSQSSS
                                                                                                       KYPLQNRLYKNSNTVRGKEFWNFESTRLSTTQISKEELSPITQDSPTSSLNMESPYLLHG
                                                                                                                                                      KI-----LFQEAPNGPGAE---
                                                                                                                                                                                                                                                        DSCLQKIPQDRPTSEVLLKHRFVLRERPPTVI-----MDLIQRTKDAVRELDNLQYRKMK
                                                                                                                                                                                                                                                                                                             DG-YNEKADIWSLGITTYELLKGLPPLSKYDPMKVMTNLPKRKPPKLQ-GPFSDAAKDFV
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; Pred. No. 6.9e-14;
67; Mismatches 129;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
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BY SIMILARITY.

N -> NVN (IN REF. 2).
G -> R (IN REF. 2).
W; 6143055E85BAF4FF CRC64;
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Job time: 22.3915 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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SPTREMBL_21:*

1: Sp_archea:*
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3: sp_fungl:*
4: sp_human:*
5: sp_invert
6: sp_mammal
7: sp_mhc:*
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5140
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Gapop 10.0 , Gapext 0.5
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sp_mammal:*
sp_mhc:*
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sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
 sp_rodent:*
sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	8	7	σ	U	4	ω	2		Result No.
735.5	778	1413	1841.5	2385.5	2427.5	2432.5	2442.5	2445.5	2802.5	2805.5	2812.5	3530	3785.5	4676	5054	Score
14.3	15.1	27.5	35.8	46.4	47.2	47.3	47.5	47.6	54.5	54.6	54.7	68.7	73.6	91.0	98.3	Query Match I
1305	438	398	1039	898	898	898	898	898	1001	1001	1005	1062	1049	1235	1235	Length I
4	0	4	Ģ	4	13	4	4	4	4	11	4	4	4	4	11	DВ
Q9UKE3	Q9BH01	Q9H7S5	Q9VWG8	Q9UHG7	Q919E0	Q9H2K8	Q9NZM9	Q9НС79	Q9H2K7	088664	Q9P2I6	Q9NSW2	094957	Q9UL54	Q9JLS3	ID
Q9uke3 homo sapien	Q9bh01 macaca fasc	Q9h7s5 homo sapien	Q9vwg8 drosophila	Q9uhg7 homo sapien	Q9i9e0 gallus gall	Q9h2k8 homo sapien	Q9nzm9 homo sapien	Q9hc79 homo sapien	Q9h2k7 homo sapien	O88664 rattus norv	Q9p2i6 homo sapien	Q9nsw2 homo sapien	094957 homo sapien	Q9u154 homo sapien	Q9jls3 rattus norv	Description

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12.2	12.3	12.3	12.4	12.4	12.5	12.5	12.5	12.5	12.5	12.6	12.7	12.8	12.9	12.9	13.3	13.5	13.5	13.5	13.6	13.8	13.8	13.9	13.9	14.1	14.1
825 825 1202	1175	445	1295	1308	669	1300	497	809	1233	1235	1233	1120	836	1231	842	1323	1165	950	1268	1331	1352	473	1360	1297	1276
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Q8SAE1 Q9ARL7 Q9WU41	075172	Q60877	Q9P2R8	Q9JM52	Q8T0S6	Q9JM92	Q9JI10	Q8VYC1	054988	Q9H2G2	P97820	Q9LQA1	024527	055092	Q9FNU3	Q9UKEO	095819	Q9YHC9	Q9UKD8	Q9UKE4	Q9UKE2	Q91VG7	Q9UKE5	Q9UKD9	Q9UKE1
Q8sael triticum mo Q9arl7 hordeum vul Q9wu41 mus musculu	homo	Q60877 mus musculu	homo		s6 dros	mus	Q9ji10 mus musculu	ara	O54988 mus musculu		P97820 mus musculu		024527 arabidopsis	O55092 cavia porce	Q9fnu3 oryza sativ	Q9ukeO homo sapien	095819 homo sapien	Q9yhc9 xenopus lae	homo	homo	-	Q91vg7 mus musculu	homo	Q9ukd9 homo sapien	Q9ukel homo sapien

## ALIGNMENTS

R R R R R R R R R R R R R R R R R R R	RESULT Q9JLS3 ID Q0 AC QDT
	LT 1  (99/ILS3 PRELIMINARY; PRT; 1235 AA. (99/ILS3; Q9/ILS3; Q1-OCT-2000 (TrEMBLrel. 15, Created) (10-OCT-2000 (TrEMBLrel. 20, Last sequence update) (11-MAR-2002 (TrEMBLrel. 20, Last annotation update) (12-Mar-2002 (Tremblarel. 20, Last annotation update) (13-Mar-2002 (Tremblarel. 20, Last annotation update) (14-Marmyala; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; (15-Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. (16-Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. (17-Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. (18-Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. (19-Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. (19-Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. (19-Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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PROSITE; PS00
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SEQUENCE 12
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EEEEEEEEGGAPIGTPRDPGDGCPSPDIPPEPPPSHLRQYPASQLPGFLSHGLLTGLSFA
                                           DISKEMKESRVPSLASQERNIIGQEEAGAWNLWEKEHGNLVDMEFKLGWVQGPVLTPVPE
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                                                                                                    EAILGQRMLGEEEEAVPERMILGKEGTTLEPEEQRILQEEMGTFSSSPQKHRSLVNEEDW
                                                                                                                                                EYNKRREQELRQKHAAQVRQQPKSLKVRAGQLPMGLPATGALGPLSTGTLSEEQPCSSGQ
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                                                                                                                                                                                                                                                                                      AEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEEL
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                                                                                          EAILGQRMLGEEEEAVPERMILGKEGTTLEPEEQRILGEEMGTFSSSPQKHRSLVNEEDW
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                                                                                                                                    EYNKRREQELRQKHAAQVRQQPKSLKVRAGQLPMGLPATGALGPLSTGTLSEEQPCSSGQ
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PS50011); PROTEIN_KINASE_DOM; 1.
PS00108; PROTEIN_KINASE_ST; 1.
PS00108; PROTEIN_KINASE_ST; 1.
ing; Kinase; Serine/threonine protein kinase; Transferase; 1235 AA; 138750 MW; 426960D0812518AD CRC64;
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C Q9UL54;

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Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR00109; pkinase; 1.
PF100000; PF1000001; Euk_pkinase; 1.
PF10000001; Euk_pkinase; 1.
PF10000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PR0SITE; PS00107; PROTEIN_KINASE_DOW; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-prot SEQUENCE 1235 AA; 138232 MW; 3AB9E8E66
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J. Biol. Chem. 275:4311-4322(2000)
-- SIMILARITY: BELONGS TO THE SER
EMBL; AF061943; AAD45816.1; -.
HSSP; P24941; LB38.
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TISSUE-BRAIN;
MEDLINE-99156230; PubMed=10048485;
Magase T. Ishikawa K., Suyama M., Kikuno R.
Miyajima N., Tanaka A., Kotani H., Nomura N.
"Prediction of the coding sequences of unide
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DNA Res. 5:355-364(1998).
The complete sequences for large proteins in DNA Res. 5:355-364(199[2]]
SEQUENCE FROM N.A. Yustein J.T., Robinson Characterization of a Selectively Activate p dependent Mechanism.";
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Mammalia; Eutheri
NCBI_TaxID=9606;
[1]
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Pfam; PF00069; PKINASE; PROUDON; EUK_PKINASE; PRODON; EUK_PKINASE; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_DM; 1.

PROSITE; PS00108; PROTEIN_KINASE_DM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transport to the straight of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEGPESREMAMMQEGEHTVTSHSSIIHR
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SFYGTPYWMAPEVILAMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
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Pred. No. 1.9e-
35; Mismatches
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.9e-211;
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Pfam; PF00069; pkinase; 1.
ProDom; PD0000001; Euk_pkinase; 1.
ATP-binding; Hypothetical protein; Transferase.
SEQUENCE 1062 AA; 118780 MW; A4BZB359EEC9CAAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2000) to the EMBL; AL137701; CAB70882.1; HSSP; P02649; 1NFO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 118.8 kDa protein.
DKFZP434N1427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wiemann S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bloecker H.,
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                                                                                                                                                                                                      HREVLRERPETVIMDLIQRTKDAVRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEP 337
              EREEHSGRLQRELEAQRAGFGTEAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKE 577
                                                               RRAYCRNRDHFATIRTASLVSRQIQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRG
                                                                                                                  SREMAMMQEGEHTVTSHSSIIHRLPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSSAR 457
                                                                                                                                                                   YMHRAGTLTSLESSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEEFPE
                                                                                                                                                                                                                                                         EREEHSARLQRELEAQRAGFGAEAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKE
                                                                                                   AREMAMMQEGEHTVTSHSSIIHRLPGSDNLYDDPYQPEITPSPLQPPAAPAPTSTTSSAR
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695; Conserv
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                                                                                                                                                                                                                                                                                                                      68.7%;
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                                                                                                                                                                                                                                                                                                                      Score 3530; DB 4; Pred. No. 1.3e-196;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ (-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY (EMBL; AM037782; BAA92599.1; -EMBL; AY049015; AAL12217.1; -. HSSP; P24941; 1B38.
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O9P2I6; Q9E175;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
KIAAI361 protein (Serine/threonine kinase TAO1) (Fragment).
                                     Prodom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S.TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
                                                                                                                                                                                                                                                                                                      MEDLINE-20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human
The complete sequences of 150 new cDNA clones from brain w
for large proteins in vitro.";
DNA Res. 7:65-73(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                        InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
              NON_TER
                          ATP-binding; Kinase;
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                        Serine/threonine-protein kinase; Transferase
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A83BD4E53569BCB5 CRC64;
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--HWGHPMGGPPQAWGHPMQGGPQPWGHPSGP
                   EEEGGAPIGTPRD----PGDGCPSPDIPPEPP
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                                                              LASQERNIIGQEEAGAWNLWEKEH--GNLVDMEFK-----
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Pred. No. 5.3e-155;
4; Mismatches 197;
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MEDLINE=99003202; PubMed=9786855;
Hutchison M., Berman K.S., Cobb M.H.;
Hutchison M., Berman K.S., Cobb M.H.;

"Isolation of TAO1, a protein kinase that ac
activated protein kinase cascades.";
J. Biol. Chem. 273:28625-28632(1998).

"I- SIMILARITY: BELONGS TO THE SER/THR FAMIL
EMBL; AF084205; AAC71014.1; -..
EMBL; AF084215; 1B38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; (Mammalia; Eutheria; 1) NCBI_TaxID=10116; [1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase; 1.
Probom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S. TKC; 1.
SMART; SM00220; S. TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-pro
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InterPro; IPR002290; Ser_thr_pkinase.
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QMQEHEQDSELREQMSGYKRMRRQHQKQLMTLENKLKAEMDEHRLRLDKDLETQRNNFAA
                                                                                                                                                                                                                    ASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEEGPESREMAMMQEGEHTVTSHSSIIHR
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                                                                                                                                                                                                                                                                                                                                                                                   ESPTLQSNEWSDYFRNFVDSCLQKIPQDRPTSEELLKHMFVLRERPETVLIDLIQRTKDA
                                                                                                                                                                                             ASSQSSSVNSLPDASDDKSELD-----
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1001 AA; 115952 MW; 85511B62DBD62FCC CRC64;
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Pred. No. 1.3e-154;
B; Mismatches 225;
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Sciurognathi;
                                                                                            -QVSRHKSHYRNREHFATIRTASLVTR
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EMEKLIKKHQASMEKEAKVMANEEKKFQQHIQAQQKKELNSFLESQKREYKLRKEQLKEE

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RESULT 7

Q9H2X7

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                                                                                                                                                                Yustein J.T., Robinson D., Kung H.-J.;
Yustein J.T., Robinson D., Kung H.-J.;
Yustein J.T., Robinson D., Kung H.-J.;
Yuharacterization of a Subfamily of Human ST
Selectively Activate p38 Through MKK3 and ar
dependent Mechanism.";
Submitted (MAY-2000) to the EMBL/GenBank/DDB
EMBL; AF563312; AAG38502.1; -.
HSSP; P24941; 1B38.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                            Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
STE20-like kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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7F0E534D3E7E159E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGGAPIGTPRD----PGDGCPSPDIPPEPP
                                                                                                ELLNAYQSKIKMQAEAQHDRELRELEQRVSLRRALLEQKIEEEMLALQNECTE-RIRSLL
                                                                                                                                                                                                                  LEYNKRREQELRQKHAAQVRQQPKSLKVRAGQLPMGLPATGALGP-----
                                                                                                                                                                                                                                                                                                       LNENQSTPKKEKQEWLSKQKENIQHFQAEEEANLLRRQRQYLELECRRFKRRMLLGRHNL
                                                                                                                                                                                                                                                                                                                                                     EMEKLIKKHQAAMEKEAKVMSNEEKKFQQHIQAQQKKELNSFLESQKREYKLRKEQLKEE
                                                                                                                                                                                                                                                                                                                                                                     EAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEE
                                                                                                                                                                                                                                                                                                                                                                                                        QMQEHEQDSELREQMSGYKRMRRQHQKQLMTLENKLKAEMDEHRLRLDKDLETQRNNFAA
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                                                ERQAREIEAFDSESMRLGFSNMVLSNLSPEAFSHSYPGASGWSHNPTGGPGP-
                                                                        SQERNIIGQEEAGAWNLWEKEH--GNLVDMEFK-----LGWVQGPVLTPVPEEEEEEEE
                                                                                                                                                   KSEHKAVLKRLKEEQTRKLAILAEQYDHSINEMLSTQALRLDEAQEAECQVLKMQLQQEL
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                                                                                                                                                                         EQPCSSGQEAILGQRM-LGEEEEAVPE--RMILGKEG
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Pred. No. 2e-
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Best Local S
Matches 505
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PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00219; TYFKC; 1.

SMART; SM00219; TYFKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE; UNKNOWN_1.

ATP-binding; Kinase; Transferase.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=20384190; PubMed=10924369;
Zhang W., Chen T., Wan T., He L., Li N., Yuan Z.,
"Cloning of DPK, a novel dendritic cell-derived pr
"Cloning of DPK, a novel dendritic cell-derived pr
"cloning of the ERK1/ERK2 and JNK/SAPK pathways.";
activating the ERK1/ERK2 and JNK/SAPK pathways.";
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Q9HC79;
01-MAR-2001
01-MAR-2001
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01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Serine kinase (STEO-like Kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N. TISSUE=PLACENTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001245; InterPro; IPR000130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000719;
InterPro; IPR002290;
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L; BC002756; AAG0756.1; -

2; BC4941; 1B38.
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THEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLQYRKMKKILFQEAPNGPGAEAPEEEEEEAEPYMHRAGTLTSLESSHSVPSMSISASSQS
                                                                                                                                                                                        QSNEWTDSFRRFVDYCLQKIPQERPTSAELLRHDFVRRDRPLRVLIDLIQRTKDAVRELD
                                                                                                                                                                                                                                                           PYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSPTL
                                                                                                                                                                                                                                                                                    PYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPAL
                                                                     NLQYRKMKKILFQETRNGPLNESQEDEEDSEHGTSLNREMDSLGSNHSIPSMSVSTGSQS
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; Ser_thr_pkinase.
; Tyr_pkinase.
; Zn_MTpeptdse.
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01-OCT-2000 (TrEM
01-OCT-2000 (TrEM
01-MAR-2002 (TrEM
Serine/threonine
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Carter T.G., Benton B., Fruhling D., Monks C.R.F., Windm Carter T.G., Manfredi J., Johnson G.L., Pleiman C.M.; Kupfer A., Manfredi J., Johnson G.L., Pleiman C.M.; Windm Y.D. A., Manfredi J., Johnson G.L., Pleiman C.M.; Windm Y.D. A., Manfredi J., Johnson G.L., Pleiman C.M.; Windm Y.D. A., Windm Y.D. 
                 PRINTS; PRO0109; TYRKINASE.
Prodom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINA.
PROSITE; PS50011; PROTEIN_KINA.
                                                                                                                                                   InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000130; Zn_MTpeptdse.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NZM9
                                                                                                                                          Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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Metazoa; Chordata; C
Metazoa; Primates; (
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2 (TrEMBLrel. 20,
eonine kinase.
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                   PROTEIN_KINASE_ATP;
PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence up
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PROTEIN KINASES

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Best Local Sim
Matches 504;
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ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase SEQUENCE 898 AA; 105432 MW; 9738BD5DCFA12AC9 CRC64;
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 REI---
                   RNIIGQEEAGAWNLWEKEHGNLVDMEF
                                      NAYQSKIKMQTEAQHERELQKLEQRVSLRRAHLEQKIEEELAALQKERSERIKNLLERQE
                                                                               ILKTLKDEQ----TRKLAILAEQYEQSINEMMASQALRLDEAQEAECQALRLQLQQEMELL
                                                                                                     -TGTLSEEQPCSSGQEAILGQRMLGEEEEAVPERMILGKEGTTLEPEEQRI-LQEEMGTF
                                                                                                                          RERELHRKHVMELRQQPKNLKAMEMQIKKQFQDTCKVQTKQYKALKNHQLEVTPKNEHKT
                                                                                                                                     EDLNKKQTOKDLECALLLRQHEATRELEURQLQAVQRTRAELTRLQHQTELGNQLEYNKR
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ETFDMESLRMGFGNLVTLDF
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                                                             SSPQKHRSL-----
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Pred. No. 1.4e
.30; Mismatches
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1.4e-133;
hes 210;
                                                             -VNEEDWDISKEMKESRVPSLASQE
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Best Local Similarity
Matches 502; Conserv
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PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SNART; SM00220; S_TKC; 1.

SNART; SM002219; TYFKC; 1.

SNART; SM00219; TYFKC; 1.

PROSITE; PS00101; PROTEIN_KINASE_ATD; 1.

PROSITE; PS0011; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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Q9H2K8;
01-MAR-2001 (TrEMBI
01-MAR-2002 (TrEMBI
01-JUN-2002 (TrEMBI
STE20-like kinase (
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NON_TER
SEQUENCE
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000130; Zn_MTpeptdse.
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"Characterization of a Subfamily of Human STE2
Selectively Activate p38 Through MKK3 and are
dependent Mechanism.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
EMBL; AFC63311; AAG38501.1;
HSSP; P24941; 1B38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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HVF---IRDEAGHGDPRPEPRPTQSVQSQA----LHYRNRERFATIKSASLVTRQIHEHE
                                                                                                      SSVNSLADASDNEEEEEEEEEEEEEEEEEEEEGPESREMAMMQBGEHTVTSHSSIIHRLPGSD
                                                                                                                                                                                                                                                                                                                                                            PYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPAL
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                                                                                     SSVNSMQEVMDE
                                                                                                                                                                                                                                                                                                                                         PYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSPTL
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868
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 130;
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.3%; Score 2432.5; 54.2%; Pred. No. 5.1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; I
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                  SSSELVMMHDDESTINSSSSVVHK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; DB 4;
5.1e-133;
hes 212;
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Query Match
Best Local Similarity
Matches 504; Conser
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Gallus gallus (Chicken).
                                                                                                       Pfam; PF00069; pkinase; 1.

ProDom; PD00001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-20162342; PubMed-10698516;
YUStein J.T., Li D., Robinson D., Kung H.
"KFC, a Ste20-like kinase with mitogenic
                                                                                                                                                                                                                                                                                                                                           Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                  InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                      activate the SAPK/JNK pathway."; Oncogene 19:710-718(2000).
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lus gallus (Chicken).
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                                                                                  AA;
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                                                                                 105289 MW;
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Last sequence update)
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                          Score 2427.5; DB 13
Pred. No. 1e-132;
7; Mismatches 216;
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; Galliformes; Phasianidae; Phasiani
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RESULT Q919E0

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Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001130; Zn_MTpeptdse.
Pfam; PF00069; pkinase; 1.
Pfam; PF000001; Euk_pkinase; 1.
PRINTS; PR001109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.
PROSITE; PS001142; ZINC_PROTEASE; UNKNOWN_1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. BIOL. Chem. 274:3328/-33280;; ...; SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES EMBL; AF119867; AAF14559.1; -.
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MEDLINB=20026851; PubMed=10559204;

MEDLINB=20026851; PubMed=10559204;

Tassi E., Biesova Z., Di Fiore P.P., Gutkind J.S., V

"Human JIK, a novel member of the STE20 kinase family

JNK and is negatively regulated by epidermal growth

J. Biol. Chem. 274:33287-33295(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding; Kinase; Serine/threonine-protein kinase; SEQUENCE 898 AA; 105657 MW; 61F04628713E6025 CRC6
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Mammalia; Eutheria;
    513
                                546
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KKQVAIIEKEAKVAAADEKKFQQQILAQQKKDLTTFLESQKKQYKICKEKIKEEMNEDHS
                RRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEELQENPS
                                                                            NLYDDPYQPEMTPGPLQPPAAPPTSTSSSSARRRAYCRNRDHFATIRTASLVSRQIQEHE
                                                                                                                                                                                                                                                                   NLQYRKMKKILFQEAPNGPGAEAPEEEEEEAEPYMHRAGTLTSLESSHSVPSMSISASSQS
                                                                                                                                                                                                                                                                                                               PYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSPTL
                                                                                                                                                                                                                                                                                                                                                                                          PYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQ
                                                            QENELREQMSGYKRMRRQHQKQLIALENKLKAEMDEHRLKLQKEVETHANNSSIEI
                                                                                                                                                                                                                  SSVNSLADASDNEEEEEEEEEEEEEEEEEGPESREMAMMQEGEHTVTSHSSIIHRLPGSD
                                                                                                                                                                                                                                                  NLQYRKMKKILFQETRNGPLNESQEDEEDSEHGTSLNREMDSLGSNHSIPSMSVTWN---
                                                                                                                                                                                                                                                                                                                                           QSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELD
                                                                                                                                                                                                                                                                                                                                                                                                                                     VEIAAITHGALHGLAYLHSHALIHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKGVLKDPEIADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTSEVVAIKKMSYSGKQ
                                                                                                                        - IRDEAGHGDPRPEPRPTQSVQSQA----LHYRNRERFATIKSASLVTRQIHEHE
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                                                                                                                                                                                      -QPEQGNGQPGQQPFHSKHVRVMMHDDESTINSSSSVVHK---KD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2385.5; DB 4
Pred. No. 2.7e-130;
3; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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RESURUTATION OF THE PROPERTY O
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S.A., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Meinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ДЬ
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Q9VWG8;
01-MAY-2000
01-MAY-2000
01-MAR-2002
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso-
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
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RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
DR EMBL, AE003512; AAF48973.1; -.
DR EMBL, AE003512; AAF48973.1; -.
DR HSSP; P24941; 1B38.
DR FlyBase; FBgn0031030; CG14217.
DR FlyBase; FBgn0031030; CG14217.
DR InterPro; IPR000290; Ser_thr_pkinase.
DR InterPro; IPR000290; Ser_thr_pkinase.
DR Ffam, PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
KW ARP-binding; Transferase.
SC SEDIEMCE 11030 AA. 118208 MG. 3010157167208F34 CD664.
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                                                                                SRLRGEREEHSGRLQRELEAQRAGFGTEAEKLARRHQAIGEKEARAAQAEERKFQQHILG
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                                                                                                                                               MQEGEHT----VTSHSSIIHR----LPGSDNLYDDPYQP----EMTPGPLQPPAAPPT---
                                                                                                                                                                                                                                                                                                                                                                                                                    VRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRAGTLT---SLESSHSVPSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESPTLPKNDWSDAFCSEVELCLKKMPAERPSSAKLLTHAYVTRPRSDTVLLELIARTKSA
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                                QQKKELAALLEAQKRTYKLRKEQLKEELQENPSTPKREKAEWLLRQKEQLQQCQAEEEAG
                                                                                                                            QQAISNAVNDHGPNNFATIRTTSIVTKQQKEHMQEE-MHEQMSGYKRMRREHQAHLVKLE
                                                                                                                                                                                            LPHLSAMGHVGGGGTGTGGSGGGSPASGGPLADRIQPVQPRYLTTPAAQAAVYAASSASS
                                                                                                                                                                                                                                                              -QQGQPVPPGAVSRNSSRHRNRPPLPNIMHSMNNNVTPTNSASVVPAPAPAPAPVLPPPISV
                                                                                                                                                                                                                                                                                                                           {\tt GVSAASSQSSSSNSIPAAAQNHHHIAAHHHQQAASAAVAAAMHHHHHPHQQPPPSWPSG-}
                                                                                                                                                                                                                                                                                                                                                            SIS-ASSQSSSVNSLADASDNEEEEEEEEEEE------EEEEEEGPESREMAM
                                                                                                                                                                                                                                                                                                                                                                                         VRELDNLNYRKMKKILMVDTCETESAVGDTDDQQDD---HAGGDSSKSNSITSEHSIHSV
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Q9H7S5;
Q1+MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ14314 fis, clone PLACE3000350, weakly simil
serine/threonine-protein kinase SULU (EC 2.7.1.-).
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"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK024376; BaB14901.1;
"InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Ser_thr_pkinase.
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ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
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NFAAEMEKLIKKHQAAMEKEAKVMSNEEKKFQQHIQAQQKKELNSFLESQKREYKLRKEQ
                              GFGTEAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQ
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                                                                                                                    LVSRQIQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRGEREEHSGRLQRELEAQRA
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Q1-UN-2001 (TrEMBLrel. 17, Created)
Q1-UN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q2-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q2-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q3-DEC-2001 (TrEMBLrel. 17, Created)
Q4-DEC-2001 (TrEMBLrel. 17, Created)
Q4-DEC-2001 (TrEMBLrel. 17, Created)
Q5-DEC-2001 (TrEMBLrel. 17, Created)
Q5-DEC-2001 (TrEMBLrel. 17, Last sequence update)
Q6-DEC-2001 (TrEMBLrel. 17, Last sequence update)
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Q7-DEC-2001 (TrEMBLrel. 17, Last se
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Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA libraries.";
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                                                      AGAWNLWEKEHGNLVDMEF 885
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Search completed: November 22, 2002, 12:26:07 Job time: 60.1115 secs

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                      Issued_Patents_AA: *
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Listing first 45 summaries
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-09-311-444-8
US-09-311-230-5
US-09-340-93-5
US-09-340-93-4
US-09-340-93-4
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## ALIGNMENTS

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Matches 992
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
NAME: MAKI, DAVID J.
ACOUNTY AGENTION NUMBER: 31,392
                                                                                                                                                                                                                                                            TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/09/060,410
                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acid:
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
STREET: 6300 Columbia Center,
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Mi
APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
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                                                                                                                                                                                     LENGTH: 993 amino acids TYPE: amino acid TOPOLOGY: linear
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mes 992; Conserv
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MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
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(206) 682-6031
(70) TD NO: 4:
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Hutchinson, Michele
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Sequence 2, Application US/09060410
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Patent No. 6165461
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                                                                                               VGSSSGLLPLLLLLLLLAPRWRWLAGSTAGP
                                                                                                                                     EEEEEEEGGAPIGTPRDPGDGCPSPDIPPEPPPSHLRQYPASQLPGFLSHGLLTGLSFA
                                                                                                                                                EEEEEEEEGAPIGTPRDPGDGCPSPDIPPEPPPSHLRQYPASQLPGFLSHGLLTGLSFA
                                                                                                                                                                               DISKEMKESRVPSLASQERNIIGQEEAGAWNLWEKEHGNLVDMEFKLGWVQGPVLTPVPE
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Cobb, Melan:
Hutchinson,
  Michele
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-060-410-2
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APPLICATION NUMBER: US/09/060,410
FILING DATE: 14-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 860098.421
REFERENCE/DOCKET NUMBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 596; Conserv
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC Compatible
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LENGTH: 1001 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
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APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO I
TITLE OF INVENTION: THER
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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                          YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
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QTQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRGEREEHSGRLQRELEAQRAGFGT
                                                                                        ASSQSSSVNSLPDASDDKSELD----
                                                                                                                    ASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEEFGPESREMAMMQEGEHTVTSHSSIIHR
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1.1e-177;
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US-09-060-410-17

; Sequence 17, Application US/09060410

; Patent No. 6165461
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                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO
TITLE OF INVENTION: THER
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APPLICANT: Hutchinson, Michele
APPLICANT: Chen, Zhu
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                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                        APPLICATION NUMBER: US/O FILING DATE: 14-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center,
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GENERAL INFORMATION:

APPLICANT: BINGHAM, SHARON

APPLICANT: CASE, PATRICK

APPLICANT: LAWSON, SALLY NEALE

APPLICANT: NEWTON, RICHARD ANTHONY

APPLICANT: PIERCY, VALERIE

APPLICANT: RAUSCH, OLIVER LARS

APPLICANT: RAVAL, PRAVIN

APPLICANT: SANGER, GARETH JOHN

APPLICANT: SANGER, GARETH JOHN
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US-09-393-569-2
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                                                                                                                                                US-09-393-569-2
                                                                                                                                                                                                 SEQ ID NO 2
LENGTH: 1360
                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09393569 Patent No. 6277979
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/393,569
CURRENT FILLING DATE: 1999-09-10
EARLIER APPLICATION NUMBER: GB 9907261.3
EARLIER FILING DATE: 1999-03-29
EARLIER APPLICATION NUMBER: GB 9819779.1
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                      EARLIER FILING DATE: 1998-09-10
                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NEW USE FILE REFERENCE: P32261
                                                                                                                                                             TYPE: PRT
ORGANISM: HOMO SAPIENS
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                                                                       Local Sinhes 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPGVIKDPSIAALFSNKDPEQ---DLREIGHGSFGAVYFAYDKKNEQTVAIKKMNFSGKQ 64
                                   MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFFMAPEVILAMDEGHYTDRADIWSLGITCIELAERRPPLFSMNAMSALYHIAQNDPPTL
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MASDSPARSLDEIDLSAL---RDPAGIFELVELVGNGTYGQVYKGRHVKTGQLAAIKVMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPIDTSEQPEWSLEFVQFIDKCLRKPAEERMSAE
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                                                                                        Similarity
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                                                                                        13.9%;
26.2%;
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                                                                       158;
                                                                     Score 717; DB 4;
Pred. No. 2.6e-39;
58; Mismatches 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278
                                                                                                       Length 1360;
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Sequence 8, Application US/08712709 Patent No. 5863780
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                                                                                                                                                   HLRQYPASQLPGFLSHGLLT 955
                                                                                                                                                                                                                        LVDMEFKLGWVQGPVLTPVPEEEEEEEEEGGAPIGTPRDPGDGCPS-PDIP---PEPPPS 935
                                                                                                                                                                                                                                                                                                                                                                                                             KNSPGNGSALGPRLGSQPIRASNPDLRRTEP-----ILESPLQRTSS-GSSSSSSTP 736
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                                                                                                                                                                                                                                                                                                                                                                          EEQPCSS-----GQEAILGQR----MLGEEEEEAVPERMILGKEGTTLEPEEQRILQEEMGT 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVEMPRQNSDPTSENP-----PLPTRIEKFDRSSWLRQEEDIPPKVPQRTTSISPALAR 685
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                                                                                                                                                                                                                                                             RPSRPASYKKAIDEDLTALAKELRELRIEETNRPMKKVTDYSSSSEES---
                                                                                                                                                                                                                                                                                                                                      SSQPSSQGGSQPGSQAGSSERTRVRANSKSEGSP---VLPHEPAKVKPEESRDI-----T 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLDQDLLREDLNKKQTQKDLECALLLRQHEATRELELRQLQAV-----QRTRAELTRLQH 712
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Filed Herewith ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: MOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
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402 AMMQEGEHTVTSHSSIIHRLPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSARRRAY 461
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                                                                                                                                                                                                                                       239 QNESPALQSGH-WSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRT 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 169; Conserv
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                                                                                                                                                                                                                                                                                                                                                               LTEDEIATILQSTLKGLEYLHFMRKIHRDIKAGNILLNTEGHAKLADFGVAGQLTDTMAK 180
                                                                                                                                                                                                                                                                                                                                                                                                  LQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAP 178
                                                                            -GTLTSLESSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEEPGPESREM 401
                                                                                                                                                          KDAVRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRA----------
                                                                                                                                                                                                                                                                                                                       ANSFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ESDLQEIIKEISIMQQCDSPHVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKT 120
                                       DGANTMIEHDDTLP-----SQLGTMVINAEDEEEEGTMKRRDETMQPAKPSFLEY
                                                                                                                     MDVKLKRQESQQREMDQ-------DDEENSEEDEMDSGTMVRAVGDEMGTVRVASTMT 348
                                                                                                                                                                                                  TNPPPTFRKPELWSDNFTDFVKQCLVKSPEQRATATQLLQHPFVRSAKGVSILRDLINEA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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US-09-111-444-8
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GENERAL INFORMATION:
APPLICANT: Au-Young
APPLICANT: Au-Young
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
123 LQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 FEQKEKENQINSFGKSV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3174 POR CITY: Palo Alto
                                                                                                                                                                                                                                                                                              LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
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                                                                                                                                              LKDPDVAELFFKDD-----PEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSG 63
                                                   ---ESDLQEIIKEISIMQQCDSPHVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EREEHSGRLQRELEAQRAGFGTEAEKLARRHQ 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRNRDHFATIRTASLVSRQIQEHEQDSALREQLSGYKRMR----RQHQKQLLALESRLRG
                                                                                     KQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKP 122
                                                                                                                       LRNPPRRQLKKLDEDSLTKQPEEVFDVLEKLGEGSYGSVYKAIHKETGQIVAIKQVPV--
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Guegler, Karl J.
Hawkins, Phillip R.
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                                                                                                                                                                                        87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0118
                                                                                                                                                                                       Score 614; DB 3; 1
Pred. No. 4.8e-33;
7; Mismatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----IPQDGDYEFLKSWTVEDLQKRLLALDPMMEQ 457
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                                                                                 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN
NUMBER OF SEQUENCES: 9
                                                                                                                                       TELEPHONE: 415-855-0555
                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 31/.
CTTY: Palo Alto
 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CO
OPERATING SYSTEM:
SOFTWARE: FastSE
                TOPOLOGY: 11
                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Incyte PharmacosTREET: 3174 Porter Drive
                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/541,228
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNESPALQSGH-WSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEOKEKENQINSFGKSV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRNRDHFATIRTASLVSRQIQEHEQDSALREQLSGYKRMR----RQHQKQLLALESRLRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDAVRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRA-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMMQEGEHTVTSHSSIIHRLPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSARRRAY 461
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APPLICANT: Tyrell E. NO. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: SERIME/THREONINE KINASE
FILE REFERENCE: PHM. 70296
CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT FILING DATE: 1998-12-15
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                 US-09-211-930-5

; Sequence 5, Applic

; Patent No. 5962265
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US-09-211-930-5
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                                       SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 5
LENGTH: 431
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Best Local Similarity
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                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIEE----IRQKYQSKRQPILDAIEAKKRRQQ 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EREEHSGRLORELEAORAGFGTEAEKLARRHO 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRNRDHFATIRTASLVSRQIQEHEQDSALREQLSGYKRMR----RQHQKQLLALESRLRG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMMQEGEHTVTSHSSIIHRLPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSARRRAY 461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QNESPALQSGH-WSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRT 297
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                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09211930
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US-09-340-993-5
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APPLICANT: Tyrell E. No. 6034228ris
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REFERENCE: PHM. 70296. N1
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Best Local Similarity
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Best Local Similarity
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CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0 & US
EARLIER FILING DATE: 1997-12-19 & 1998-12-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
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  249
                                256 NEVDSCLQKIPQDRPTSEVLLKHREVLRERPPT-VIMDLIQRTK 298
                                                                                                                                                                                        140 AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
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                                                                                                                                                                                                                                                                                               QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
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                                                                                                                        AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFR 255
                                                                                                                                                                  DYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI-
                                                                                                                                                                                                                                                   SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE-GNYSKPLK 248
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                                                                                 -- KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE-GNYSKPLK
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ilarity 45.8%;
Conservative 48
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Pred. No. 8.6e-32;
Pred. No. 8.6e-32;
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; ORGANISM: Homo sapiens US-09-468-442-5
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CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: 9719920.2
EARLIER FILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 431
                                                                     NUMBER OF SEQ ID NOS: 14
SOFTWARE: FRStSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Applic Patent No. 6300098
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Best Local Similarity
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                                                                                                                                                                     CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/340,993
EARLIER FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
EARLIER APPLICATION NUMBER: US 09/211,930
EARLIER APPLICATION NUMBER: US 09/211,930
EARLIER APPLICATION NUMBER: US 09/211,930
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tyrell E. No. 6300098ris
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70296.N1
CURRENT APPLICATION NUMBER: US/09/468,442
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APPLICANT: Tyrell E. No. 6265560ris
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN STE20-LIKE STRESS ACTIVATED
TITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70272
                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI- 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKLRHPNTIQYRGCYLREHTAMLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAIKIIDL--EEAEDEIEDIQQEITVL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09468442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09152406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 594; DB 4; Length 431; 45.8%; Pred. No. 8.6e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298
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RESULT 12
US-08-852-743-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Force,
APPLICANT: Kyriak
                                                                                                                                                                                                  TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING LANGE 100: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,774
APPLICATION: 7-MAY-1996
                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 7-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bonventre, TITLE OF INVENTION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 DYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI - 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 EFVEACLNKEPSFRPTAKELLKHKFILRNAKKTSYLTELIDRYK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 NFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPT-VIMDLIQRTK 298
                                                                  TYPE: ami
                                                                                                                                                                                                                                     TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/
FILING DATE: 7-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish a Natural ADDRESSEE: Fish a Natural ADDRESSEE Fish a Natural ADDRESSEE Fish ADDR
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                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fraser, Janis K
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAIKIIDL--EEAEDEIEDIQQEITVL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE-GNYSKPLK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130;
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Pombo, Celia M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diskette
                               protein
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Pred. No. 8.6e
#8; Mismatches
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Query Match

11.5%;

Score 592;

DB 2;

Length 426;

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APPLICANT: Tyrell E. No. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70296
CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT FILING DATE: 1998-12-15
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER TILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 4
LENGTH: 426
TYPE: PRT
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US-09-211-930-4
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                                                                                                                                                                                          Matches 154;
                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 36.4 Matches 154; Conservative
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                 142 LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 197
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                                                                                                                                                                                                        Local Similarity
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                                                                                     LRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141
                                                                                                                                           DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPSMSISASSQSSSVNSLADASDNEEEEEEEEE-----EEEEF-----EEEGPESREM
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                                                                                                                           DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FQEAPNGPGAEAPEEEE----EAE-----PY--MHRAGTLTSLESSHS
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Pred. No. 1.2e-31;
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69; Mismatches 128;
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GENERAL INFORMATION:
APPLICANT: Tyrell E. NO. 6034228ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SEI
FILLE REFERENCE: PHM. 70296.11
CURRENT APPLICATION NUMBER: US/09/340,993
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09,
EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09,
EARLIER FILING DATE: 1997-12-19 & 1998-12-15
NUMBER: OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-340-993-4
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                                                                                                                      VDSCLQKIPQDRPTSEVLLKHRFVLR-ERPPTVIMDLIQRTKDAVRELDNLQYRKMKKIL 316
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                                                                                                                                                                                                                                                                                                           LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 197
                                            KQSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKNSPPTLEGQH-SKPFKEF
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·EGHGEESSSEDSDIDGEAEDGEQGPIWTFPPTIRPSPHSKLHKG---TALHSSQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 592; DB 3; Length 426; Pred. No. 1.2e-31;
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US-09-185-370-2
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US-09-185-370-2
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Best Local Similarity
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                                                                                                                                                                                                                                     Matches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 078
RELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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APPLICANT:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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 198 DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF 257
                                131 LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI--- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 225 | CITY: Boston
                                                                                                73 CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY 130
                                                                                                                                     83
                                                                                                                                                                  15 DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ 72
                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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Pombo, Celia M.
                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.2e-31;
9; Mismatches 128;
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                                                                                                                                                               VEACLNKDPRFRPTAKELLKHKFITRYTKKTSFLTELIDR-----YKRWKS--
                                                                                                                                                                                         VDSCLQKIPQDRPTSEVLLKHRFVLR-ERPPTVIMDLIQRTKDAVRELDNLQYRKMKKIL 316
                                                                                                         ----EGHGEESSSEDSDIDGEAEDGEQGPIWTFPPTIRPSPHSKLHKG---TALHSSQK
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Search completed: November 22, 2002, 12:28:02 Job time: 28.096 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA199.DAT: *
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AAB40294
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2184.436 Million cell updates/sec
                                                                                                                                                                                                                                                                                     Description
                                                Human/Murine SULU3
Novel human protei
Rat TAO1 kinase.
                                                                                                                             Human kinase (PKIN
Human KDS2 protein
Human ORFX ORF58 p
                                                                                                                                                                                                         Rat TAO2 kinase.
Human ORFX ORF1427
                                                                                                                                                                                                                                                                                                                                                                                                                                          to have a being printed,
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672	673.5	676	679.5	682	691.5	692	<b>N</b> )	692.5	695	696	698.5	701	708.5	709	717	717	721	722.5	723	735.5	740	765.5	777	816.5	1119	1119	1337.5	1413	1416.5	~1	1841.5	2408	2432.5	437
13.1	13.1	•	•	•	•	•	•	•	•		13.6	•		•	13.9	•	14.0	14.1	14.1	14.3	14.4		•	•		•	•	•	•	•	•	46.8		
1165	824	1297	1212	912	1324	1165	1135	911	968	1239	1339	1269	1332	1353	1360	1360	1385	1298	1277	1306	256	453	438	363	265	265	323	398	982	786	1039	899	898	898
21	23	20	22	20	22	22	21	20	20	20	22	22	22	22	22	21	22	22	22	22	21	22	22	22	22	22	22	22	20	20	22	21	20	21
AAB43016	027	AAY55932	AAE04368	AAY55939	AAB68221	ABG17470	AAY68784	AAY55957	AAY55966	AAY55931	AAM78421	AAB68223	AAB68217	AAB68219	AAB50059	AAY85263	AAM79405	AAB68222	AAB68220	AAB68218	AAB42388	AAM25915	AAG78656	AAM90795	AAU17256	AAU87435	AAU87114	589	9	93	1	319	AAY55936	424
Human ORFX ORF2780	Human lung specifi	Human ZC2 protein.	Human kinase (PKIN	Human GEK2 protein	Amino acid sequenc	Novel human diagno	Amino acid sequenc	Mouse STE20-relate	. Full length human	Human ZCl protein.	Human protein SEQ	Amino acid sequenc		Amino acid sequenc	Large NIK-Related	Human protein kina	Human protein SEQ	Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	Human ORFX ORF2152	Human protein sequ	Human serine/threo	Human immune/haema	Novel signal trans	Novel central nerv		Human protein sequ	Nematode STE20-rel		Drosophila melanog		w	Human cell signall

## ALIGNMENTS

RESULT 1
AAY49897
ID AAY4

AAY49897 standard; Protein; 993 AA

Rat TAO2 kinase

27-JAN-2000 (first entry)

AAY49897;

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TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder;
                   WPI; 1999-633831/54.
N-PSDB; AAZ32436.
                                                Cobb M,
New polypeptides that phosphorylate kinase,
                                                                                      14-APR-1998;
                                                                                                          14-APR-1999;
                                                                                                                            21-OCT-1999
                                                                                                                                                WO9953076-A1
                                                                                                                                                                  Rattus sp.
                                                                                                                                                                                      neurodegeneration; MAP kinase; MAP/ERK kinase
                                                                  (TEXA ) UNIV TEXAS SYSTEM.
                                                Hutchison M,
                                                                                       98US-0060410
                                                                                                          99WO-US08165
                                                Chen Z,
                                                 Berman
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 used to screen
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Human KDS1 serine/ Murine SULU3 prote

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Best Local S
Matches 992
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               QDLLREDLNKKQTQKDLECALLLRQHEATRELELRQLQAVQRTRAELTRLQHQTELGNQL
                                                                                   QENPSTPKREKAEWILLRQKEQLQQCQAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLD
                                                                                                                                                                                                                                                                                                                                          ASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEEEEEFPESREMAMMQEGEHTVTSHSSIIHR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPLQEVELAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN 180
                                                                                                                                                      AEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEEL
                                                                                                                                                                                                                                                                                                                                                                                                                               VRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEEAEPYMHRAGTLTSLESSHSVPSMSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
QDLLREDLNKKQTQKDLECALLLRQHEATRELELRQLQAVQRTRAELTRLQHQTELGNQL
                                                                   QENPSTPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLD
                                                                                                                                   AEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEEL
                                                                                                                                                                                                    IQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRGEREEHSGRLQRELEAQRAGFGTE
                                                                                                                                                                                                                        IQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRGEREEHSGRLQRELEAQRAGFGTE
                                                                                                                                                                                                                                                                                          LPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSARRRAYCRNRDHFATIRTASLVSRQ
                                                                                                                                                                                                                                                                                                                                                                                                               VRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRAGTLTSLESSHSVPSMSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
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                                                                                                                                                                                                                                                                        LPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSARRRAYCRNRDHFATIRTASLVSRQ
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antinamentc; gene therapy; cancer; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma, allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; open reading frame; OREX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                             Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                        Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
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                                                                                                                  neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
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DB; AAC75872.
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Claim 11; Page 2092-2095;

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antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; cimmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; coagulant; vasotropic; coagulant; vasotropic; coagulant; proteinsive; dermatological; immunosuppressive; coantininflammatory; antibacterial; antiviral; antifungal; antirheumatic; coantithyroid; and antianaemic. The sequences can be used for determining coagulant; conditions associated with an ORFX-associated disorder. The presence of or predisposition to, or preventing or treating coagular cardiscal conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy certors. The proteins and nucleic acids may be used to treat concers, cordiferative disorders, neurodegenerative disorders, osteoarthritis, collectors. The proteins and nucleic acids may be used to treat concers, cordiferative disorders, osteoarthritis, collectors, hypothyroldism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, collectorial or fungal infection, malaria, autoimmune disorders, asthma, allegatic anaemia burner.
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Matches 913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
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                                                                                                             QENPSTPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLD
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                                                                              QENPSTPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLD
                                                                                                                                                                                           AEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEEL
                                                                                                                                                                                                                                                                                                                                                        IQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRGEREEHSGRLQRELEAQRAGFGTE
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Pred. No. 7.7e-289;
3; Mismatches 40;
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14-JAN-2000;
21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human kinase; PKIN-7; therapy; immune disorder; Addison's disease; AIDS; acquired immune deficiency syndrome; growth and developmental disorder; arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma; leukaemia, cardiovascular disease; myocardial infarction; hypertension; lipid disorder; cancer; fatty liver; cholestasis; transgenic animal; gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological; antidiabetic; nephrotophic; antilcer; antiarthritic; antirheumatic; antipscriatic; neuroprotective; cytostatic; hepatotrophic; osteopathic; vasotropic; antianginal; anorectic.
  N-PSDB; AAD08640
                          WPI; 2001-418059/44.
                                                                          Yang J,
Yao MG,
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30..26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), and myelofibrosis; cancers such as adenocarcinoma and leukaemia, cardiovascular diseases such as myocardial infarction and hypertension; and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is useful to detect upstream sequences such as promoters and regulatory elements, for creating knock in or knock out in humanised animals or transgenic animals to model human disease and for somatic or germline gene therapy for treating the above mentioned disorders. The present sequence is human kinase (PKIN)-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human kinase proteins (PKIN) useful for diagnosing, treating, preventing immune disorders, cardiovascular diseases and disorders affecting growth and development associated with abnormal expression
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AEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEEL
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                                                                                      IQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRGEREEHSARLQRELEAQRAGFGAE
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cDNA library. A clone (see AAX07074) encoding KDS1 (see AAW97676) was also obtained. Both KI

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                                                                             31; Page 85-88; 100pp; English.
                                                                                                    signal transduction processes
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                      QENPSTPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLD
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EYNKRREQELRQKHAAQVRQQPKSLKKKTNTNKIPEPA
                                                                              QDLLREDLNKKQTQKDLECALLLRQHEATRELELRQLQAVQRTRAELTRLQHQTELGNQL
                                                                                                      QENPSTPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLD
                                                                                                                                                                                                                                                     AEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEEL
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                                                                                                                                                                                                                                                                                                                                                                                  IQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRGEREEHSGRLQRELEAQRAGFGTE
                                                                                                                                                                                                                                                                                                                                                                                                                            LPGSDNLYDDPYQPEITPSPLQPPAAPAPTSTTSSARRRAYCRNRDHFATIRTASLVSRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPLQEVETAAVTHGAVQGLAYLQSHNMTHRDVKAGNTLLSEPGLVKLGDFGSASIMAPAN
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96.0%;
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Pred. No. 8
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8.4e-229;
nes 18;
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, completely which represent the human ORFX open reading frames 1 to 3161. The ORFX open preading frames 1 to 3161. The open present frame frames open preading frames open pressive; antidiabetic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating open the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating concluded candidates of predistance of or predisposition to, or preventing or treating or treating or treating of the presence of or predisposition to, or preventing or treating or treating of the presence of or predisposition to, or preventing or treating or treating of the presence of or predisposition to, or preventing or treating or treating of the presence of or predisposition, and antide preventing or treating o
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05-APR-1999;
30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB40294 standard; Protein; 1062
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DB; AAC74503.
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99US-0127636.
99US-0127728.
2000US-0540763.
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                       inhibit thrombosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QAVQRTRAELTRLQHQTELGNQLEYNKRREQELRQKHAAQVRQQPKSLKVRAGQLPMG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EREEHSGRLQRELEAQRAGFGTEAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SREMAMMQEGEHTVTSHSSIIHRLPGSDNLYDDPYQPEMTPGPLQPPAAPPTSTSSSSAR 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YMHRAGTLTSLESSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEEF 397
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                                                                                                                                                                                                                                        HLRPCPASQLPGLLSHGLLAGLSFAVGSSSGLLPLLLLLLLLPLLA
                                                                                                                                                                                                                                                      HLRQYPASQLPGFLSHGLLTGLSFAVGSSSGLLPLLLLLLLLPLLA 980
                                                                                                                                                                                                                                                                                                 EDESLIDEEFELGWVQGPALTPVPEEEEEEEEE--GAPIGTPRDPGDGCPSPDIPPEPPPT
                                                                                                                                                                                                                                                                                                                                                         ILQEEMGTFSSSPQKHRSLVNEEDWDISKEMKESRVPSLASQERNIIGQEEAGAWNLWEK
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                                                                                                                                                                Peptide; 1001 AA
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Pred. No. 5e-216;
                                                                          protein sequence
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inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis; rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure; oxidative stress-related neurodegenerative disorder; Parkinson's disease; amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist; antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthm
                                                     mesangial disorder; growth regulation; wound healing; T cell activation;
immunosuppressant.
                                                                                                               ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               asthma;
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Homo sapiens sp.

WO9953036-A2

21-OCT-1999

13-APR-1999; 99WO-US08150

14-APR-1998; 98US-0081784

(SUGE-) SUGEN INC.

ė, 70, Ö

WPI; 1999-611301/52.

Novel kinase-related polypeptides used for the diagnosis and of kinase-related diseases and disorders  $\,$ treatment

Page 312-315; 387pp; English.

This sequence represents a consensus peptide sequence conained in novel CC STE20-related protein kinases. The invention relates to a nucleic acid CC molecule encoding a kinase polypeptide selected from STLK2, STLK3, STLK4, CC STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 CC sand PAK5. The proteins are used to identify agonists and antagonists, and consists and pak5. The polynucleotides, polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. treumatoid arthritis, artherosclerosis, chronic cinflammatory bowel disease (e.g. Crohn's disease), asthma, constantify, costeoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, cc and organ transplantation, chronic fifammatory pelvic disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amylotrophic lateral sclerosis, cardingsories, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth cander immunocumpresents. immunosuppressants.

Sequence 1001 AA;

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В
            Qy
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                                                                                     Query Match
Best Local S
Matches 590
121
              121
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                                          61
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                                                       KPLQEVETAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN
KPLQEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN
                                                                                            Similarity
                                                                                      Conservative
                                                                                           54.7%;
                                                                                     104;
                                                                                            Score 2812.5;
Pred. No. 2e-
                                                                                      Mismatches
                                                                                           2.5; DB 20;
2e-170;
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                                                                                      Indels
                                                                                                   Length 1001;
                                                                                     Gaps
              180
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20

181

SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN

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RRESULT 7
ABB973C
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                                               Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene t neuroprotective; antiparkinsonian; protein therapy; EST;
                                       expressed sequence
                                                                                                          Novel
                                                                                                                                    27-JUN-2002
                                                                                                                                                                                       ABB97326
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                                                                                                                                                                                                                                                                                    EEEGGAPIGTPRD----
                                                                                                                                                                                                                                                                                                            LLERQAREIEAFDSESMRLGFSNMVLSNLSPEAFSHSYPGASGWSHNPTGGPGP-----
                                                                                                                                                                                                                                                                                                                                                                   ELLNAYQSKIKMQAEAQHDRELRELEQRVSLRRALLEQK---IEEEMLALQNERTERIRS
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                                                                                                         human
                                                                                                                                                                                         standard;
                                                                                                         protein
                                                                                                                                  (first
                                                                                                                                                                                       Protein;
                                                                                                          SEQ
                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                    -PGDGCPSPDIPPEPP 933
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                                                                                                          NO:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An isolated polynucleotide for treating diseases associated encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xue
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DB; ABN32512.
             OIQEHEQDSALREQLSGYKRMRRQHQKQLLALESRLRGEREEHSGRLQRELEAQRAGFGT
                                                                                                                    ASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEGPESREMAMMQEGEHTVTSHSSIIHR
                                                                                                                                                                        VRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRAGTLTSLESSHSVPSMSIS
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                                                 KPEEEN----
                                                                LPGSDNLYDDPYQPEMTPGP-LQPPAAPPTSTSSSSARRRAYCRNRDHFATIRTASLVSR
                                                                                                      ASSQSSSVNSLPDVSDDKSELD-----
                                                                                                                                                         VRELDNLQYRKMKKLLFQEAHNGPAVEAQEEEEEQDHGVGRTGTVNSVGSNQSIPSMSIS
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Pred. No. 2e-170;
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RT;
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                                                                                                                                                                                                                                                 TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder;
                             Claim
                                               New polypeptides that phosphorylate modulators for treating e.g. cancer
                                                                                                         Cobb
                                                                                                                                             14-APR-1998;
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e present sequence represents rat TAO1 prophosphorylating MEK3 (a MAP/ERK kinase).
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Pred. No. 5.7e-
.08; Mismatches
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polypeptides, are used to screen for modulators of stress-responsive mitogen activated protein (MAP) kinase pathways. These modulators are potentially useful for treating or preventing: (1) inflammation, autoimmune disease, cancer and degeneration (inhibitors of phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders and neurodegeneration (enhancers of phosphorylation). Two kinases are also used to raise specific antibodies, useful therapeutically as modulators and as immunoassay reagents for detecting TWO kinases.

TWO kinase polynucleotides can be used: (a) for recombinant expression of TWO kinases; and (b) in the form of fragments, for detecting TWO kinase polynucleotides in standard hybridisation and amplification tests. TWO kinases are highly specific for MEK3.

2805.5; DB 2 No. 5.7e-170; 225; 20; Indels Length 103; 1001; Gaps 16;

60

YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLYWEYCLGSASDLLEVHK 120 YSGKQSTEKWQDIIKEVKFLQRIKHPNSIEYKGCYLREHTAWLVMEYCLGSASDLLEVHK 120 60

SFYGTPYWMAPEYILAMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN 180 KPLQEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN 240 180

ESPALQSGHWSEXFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA **ESPTLQSNEWSDYFRNFVDSCLQKIPQDRPTSEELLKHMFVLRERPETVLIDLIQRTKDA** 300 300

240

LPGSDNLYDDPYQPEMTPGP-LQPPAAPPTSTSSSSARRRAYCRNRDHFATIRTASLVSR -----MMEGDHTVMSNSSVIHL 479 399

KPEEEN-----YQEEGDPRTRASAPQSPP-----QVSRHKSHYRNREHFATIRTASLVTR 449 539

QMQEHEQDSELREQMSGYKRMRRQHQKQLMTLENKLKAEMDEHRLRLDKDLETQRNNFAA

EMEKLIKKHQASMEKEAKVMANEEKKFQQHIQAQQKKELNSFLESQKREYKLRKEQLKEE EAEKLARRHQAIGEKEARAAQAEERKFQQHILGQQKKELAALLEAQKRTYKLRKEQLKEE

569 599 509

659

629

EQDLVREELNKRQTQKDLEHAMLLRQHESMQELEFRHLNTTQKMRCELIRLQHQTELTNQ 689 719

LEYNKRRERELRRKHVMEVRQQPKSLKSKELQIKKQFQDTCKIQTRQYKALRNHLLETTP -EQPCSSGQEAILGQRM-LGEEEEEAVPE--RMILGKEG ----LSTGT 806 769

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RESULT 9
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This sequence represents a novel STE20-related protein kinase. The invention relates to nucleic acid molecule encoding a kinase polypeptide selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, antibodies, antibodies, antibodies, antibodies, antibodies, antibodies, antibodies, antibodies.
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                                                                                                                                                                                                                                                                    Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel protein associated with signal transduction. KDS1 has a kinase domain related to that of Ste20 (KDS1 = Kinase Domain related to Ste20). KDS1 cDNA (see AAX07074) was isolated from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 30; Page 78-81; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated vertebrate kinase - used to develop products for the diagnosis and treatment of disorders involving cellular processes such as signal transduction processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-120900/10.
N-PSDB; AAX07074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09902699-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDS1; kinase domain related to Ste20; human; serine kinase; threonine kinase; protein kinase; signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human KDS1 serine/threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW97676 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CADU-) CADUS PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-MAY-1999
                        122
                                                                    126
                                                                                                                   62
                                                                                                                                                                 66
                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription. KDS polypeptides and polynucleotides can be for treating disorders involving aberrant expression of alian KDS genes. They can also be used for detection, nosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide comprises human serine/threonine kinase KDS1,
                                              VEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGT 185
                                                                                                                                           SNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQE 125
                                                                                                                                                                                                              RKGVLKDPEIADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTNEVVAIKKMSYSGKQ
                                                                                                                                                                                                                                                            RAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQ
                        VEIAAITHGALHGLAYLHSHALIHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVGT
                                                                                                                   THEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQE
                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GL,
                                                                                                                                                                                                                                                                                                                                                                                                           898
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                           130;
                                                                                                                                                                                                                                                                                                        ; Score 2440.5;
; Pred. No. 8.2e
130; Mismatches
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                                                                                                                                                                                        Cell signalling protein-7; CSIGP-7; cell proliferation; arteriosclerosis; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;
Modified-site
                                            Modified-site
                                                                                                                                                               Addison's disease; multiple sclerosis.
                                                                                                                                                                                                                                                          Human cell signalling protein-7.
                                                                                                                                                                                                                                                                                                             28-FEB-2000
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                                                                                                                   sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNIIGQEEAGAWNLWEKEHGNLVDMEF 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAYQSKIKMQTEAQHERELQKLEQRVSLRRAHLEQKIEEELAALQKERSERIKNLLERQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -TGTLSEEQPCSSGQEAILGQRMLGEEEEAVPERMILGKEGTTLEPEEQRI-LQEEMGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RERELHRKHVMELRQQPKNLKAMEMQIKKQFQDTCKVQTKQYKALKNHQLEVTPKNEHKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TPKKEKQERISKHKENLQHTQAEEEAHLLTQQRLYYDKNCRFFKRKIMIKRHEVEQQNIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLDQDLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKQVAIIEKEAKVAAADEKKFQQQILAQQKKDLTTFLESQKKQYKICKEKIKEEMNEDHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HVF---IRDEAGHGDPRPEPRPTQSVQSQA----LHYRNREAFATIKSASLVTRQIHEHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ETFDMESLRMGFGNLVTLDF 892
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/note= "Potential phosphorylation site" 56
                                            Location/Qualifiers
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572 605 512

632

869

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452 485 425

361 365 301

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13-MAY-1998;
26-AUG-1998;
                           13-MAY-1999;
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                                         18-NOV-1999
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             98US-0085343
                           99WO-US10567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oxidative stress-related neurodegenerative disorder; Parkinson's disease; amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis; mesangial disorder; growth regulation; wound healing; T cell activation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis; rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure;
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This sequence represents a novel STE20-related protein kinase.
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                                                                                          TPKREKAEWLLRQKEQLQQCQAEEEAGLLRRQRQYFELQCRQYKRKMLLARHSLDQDLLR
                                                                                                                                          KKQVAIIEKEAKVAAADEKKFQQQILAQQKKDLTTFLESQKKQYKICKEKIKEEMNEDHS
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02-APR-1999;
05-APR-1999;
                     AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antifungal; antitheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism, SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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anticonvulsant; osteopathic; antiarthritic;
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DB; AAC77400.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathological conditions associated with an ORFX-associated disorder. The
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                                                                                                                                                                          KKQVAIIEKEAKVAAADEKKFQQQILAQQKKDLTTFLESQKKQYKICKEKIKEEMNEDHS
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Matches 391
                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                      Sequence
                                                                                                                                       The sequence data for this patent did not form specification, but was obtained in electronic f
                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 34140; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                            New isolated nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2000;
11-JUL-2000;
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                   MPAGGRAGSIKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
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MPS-ARPGSLKDPEIADLFNKHDPEKIFEDLREIGHGSFGAVYYARCNLTREIVAIKKMS
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)B; ABL13219.
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6; Mismatches 228;
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                          Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic; antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive; neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic; vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK5; STLK7; ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEX2; PAK4; PAK5; antagonist; antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma; inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
rhinitis; autoimmunity; organ transplantation; myocardial infarction; cardiovascular disease;
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Query Match
Best Local Sim:
Matches 401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stress related neurodegenerative disorders (e.g. amylotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxidative stress-related neurodegenerative disorder; Parkinson's disease; amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis; mesangial disorder; growth regulation; wound healing; T cell activation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Page 296-299; 387pp; English.
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                         SARRRAYCRNRDHFATIRTASLVSRQIQEHEQDSALREQLSGYKRMRRQHQKQLLALESR 514
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Search completed: November 22, Job time: 65.573 secs 2002, 12:23:32

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Result
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Q13043
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6 RAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQ

Query Match
Best Local Similarity
Matches 204; Conserv

Conservative

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Score 1032.5; D Pred. No. 2e-54; 7; Mismatches 1

140; DB 1;

Indels Length

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Gaps

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DOMAIN
NP\_BIND
BINDING
ACT\_SITE
SEQUENCE

982 AA;

112870 MW; 47.8%; 47.2%;

Fransterase;

Serine/threonine-protein kinase; ATP-binding.
30 289 ROTEIN KINASE.
36 44 ATP (BY SIMILARITY).
59 59 ATP (BY CTUTTONINE).

ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
745CE1E2F890977D CRC64;

ProDom; PD000001; Euk\_pkinase; 1.
SMART; SM00220; S\_TKC; 1.
PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.
PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.
PROSITE; PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.

Pfam; PF00069; pkinase;

415 19.2 842 1 CLA4 YEAST 407 18.8 1401 1 WIS4_SCHPO 394.5 18.3 626 1 M3K3_HUMAN 393.5 18.2 1501 1 NINC_DROME 388.5 18.0 626 1 M3K3_MOUSE 382 17.7 1478 1 BCK1_YEAST 373.5 17.3 618 1 M3K2_HUMAN 372.5 17.2 619 1 M3K2_HUMAN 347 16.1 1493 1 M3K1_RAT 347 16.1 1495 1 M3K1_MOUSE 365.5 16.9 506 1 NEK3_HUMAN 346 16.0 1493 1 M3K1_MOUSE
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ALIGNMENTS

## RESULT 1 SULU\_CAEEL ID SULU\_C SULU\_CAEEL STANDARD; PRT; 9 P46549; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation) WormPep; T17E9.1; CE01405. InterPro; IPR000719; Euk\_pkinase. InterPro; IPR002590; Ser\_thr\_pkinase. Pfam; PF00069; pkinase; 1. use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch). This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way Cope M.J.T.V., Kendrick-Jones A.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases. :- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. KIN-18 OR SULU OR T17E9.1. Caenorhabditis elegans. Caenorhabditis elegans. Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 16-OCT-2001 (Rel. 40, Last annotation update) Serine/threonine-protein kinase SULU (EC 2.7.1.-). EMBL; U11280; AAA19437.1; -. EMBL; U32275; AAA75370.1; -. STRAIN-Bristol N2; SEQUENCE FROM N.A. Submitted (JUN-1994) to STRAIN-Bristol N2; SEQUENCE FROM N.A. NCBI\_TaxID=6239; the EMBL/GenBank/DDBJ databases update) 982 (See http://www.isb-sib.ch/announce/ A Usage bу and for commercial

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                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=96413604; P Taylor L.K., Wang H "Newly identified s
                                                                                                                                                                                                                                                                                                                                                                                                     Q13043; Q15802; Q9NT24;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 4 (EC 2.7.1.37) (STE20-like MST1) (MST-1) (Mammalian STE20-like protein kinase 1)
(Serine/threonine protein kinase Krs-2).
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                       Submitted
                                                                                                                                                                                                                                                                            Creasy C.L., Chernoff J.; "Cloning and characterization
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=95394929; PubMed=7665586;
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                                                                                                                                 SEQUENCE OF 1-435 FROM
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                                                         MAR-2000) to the EMBL/GenBank/DDBJ databases.

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

ENZYME REGULATION: THE C-TERMINAL NON-CATALYTIC REGION INHIBJ

THE KINASE ACTIVITY.
                                   SUBCELLULAR LOCATION: Cytoplasmic (By similarity). TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
           PTM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
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SUBFAMILY
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                                                                                                                                                          Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  416
                                                                                                                                                          Sci.
                                                                                                                                                                                   H.C., Erikson R.L.;
stress-responsive p
                                                                                                                                                                                                             PubMed=8816758;
                                                                                                                                N.A.
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                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                   protein kinases,
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                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                         Hominidae;
                                                                                                                                                                                                                                                                             kinase with
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Best Local S
Matches 147
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodom: PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN KINASE_ATP; PROSITE; PS00108; PROTEIN KINASE_ST; FROSITE; PS00111; PROTEIN KINASE_TOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Genew; HGNC:11408; STK4.
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                                                                                                                                                                                                                                             RNTVIGTPFWMAPEVI---QEIGYNCVADIWSLGITAIEMAEGKPPYADIHPMRAIFMIP
FEQKEKENQINS
                              AMMQEGEHTVTS
                                                                                                                                                     KDAVRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRA----
                                                                                                                                                                                   TNPPPTFRKPELWSDNFTDFVKQCLVKSPEQRATATQLLQHPFVRSAKGVSILRDLINEA 297
                                                                                                                                                                                                               QNESPALQSGH-WSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRT
                                                                                                                                                                                                                                                             ANSFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIA 238
                                                                                                                                                                                                                                                                                                      LTEDEIATILQSTLKGLEYLHFMRKIHRDIKAGNILLNTEGHAKLADFGVAGQLTDTMAK 180
                                                                                                                                                                                                                                                                                                                        LQEVETAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAP 178
                                                                                                                                                                                                                                                                                                                                                                    ---ESDLQEIIKEISIMQQCDSPHVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKT 120
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                                                             DGANTMIEHDDTLP
                                                                                                                      MDVKLKRQESQQREVDQ
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                                                                                        -GTLTSLESSHSVPSMSISASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEGPESREM 401
                                                                                                                                                                                                                                                                                                                                                                                                 KQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity
147; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00108; PROTEIN_KINASE_ST; FALSE_NEG. PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000719; Euk_pkinase.
IPR002290; Ser_thr_pkinase.
IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein kinase; ATP-binding.
30 281 PROTEIN KINASE.
36 44 ATP (BY SIMILARITY).
59 59 ATD 'PY TILLARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pkinase;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY)
BY SIMILARITY.
POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 610.5; Db 1
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V -> M (IN REF. 1).
; 150758EBC5F77D5C
                                                            SQLGTMVINAEDEEEEGTMKRRDETMQPAKPSFLEY
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                                                                                                                        -DDEENSEEDEMDSGTMVRAVGDEMGTVRVASTMT
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RESULT

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ST25_MOUSE
ID ST25_MOUSE
ID ST25_MA
AC Q922W1
DT 16-OCT
DT STK25
OS MUSARY
OC MAMMMAIN
CC -!- SU
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                              Transferace,
Phosphorylation.
DOMAIN
20
NP_BIND
26
NP_BIND
49
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BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile stress-response kinase 1) (Ste20/oxidant stress response (SOK-1) (Ste20-like kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genetic mapping of human and mouse PAK genes.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: OXIDANT STRESS-ACTIVATED SERIME/THREONINE KINASE
MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD; MGI:1891699; Stk25.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF004934; AAD01208.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Melnick M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STK25 OR SOK1.
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                              142
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                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTOPHOSPHORYLATION. THE C-TERMINAL THE KINASE ACTIVITY (BY SIMILARITY). SUBCELLULAR LOCATION: Cytoplasmic (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
CATALYTIC ACTIVITY: ATP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENZYME REGULATION: ACTIVATED
                                                                                                                                                                                                  DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
                           LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM
                                                                      CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY
                                                                                                                   LRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141
                                                                                                                                                                 DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00108; PROTEIN_KINASE_ST; FALSE_NEG PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation being promoted to the swiss institute of Bioinformatics.
                                                                                                                                                                                                                                                                                                                                                                     140
426 .
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                     ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                     48175 MW;
                                                                                                                                                                                                                                                                                       27.6%;
36.6%;
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                                                                                                                                                                                                                                                                   68;
                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                          Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmic (By similarity)
SER/THR FAMILY OF PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                          597.5; DB 1;
No. 6.3e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tein = ADP + a phosphoprotein.
PHOSPHORYLATION, PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                426
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  (Sterile
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                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                              Length
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
    RESULT 4
STK3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                           [2]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=96413604; PubMed=8816758;
Taylor L.K., Wang H.C., Erikson R.L.;
Taylor identified stress-responsive p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STK3_HUMAN STANDARD; PRT; 491 AA.
Q13188; Q15801; Q15445;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 3 (EC 2.7.1.37) (STE20-1ike
MST2) (MST-2) (Mammalian STE20-like protein kinase 2)
(Serine/threonine protein kinase Krs-1).
                                                     -!- CATALYTIC ACTIVITY: ATP + a protein =
-!- SUBCELLULAR LOCATION: Cytoplasmic (By
-!- TISSUE SPECIFICITY: EXPRESSED AT HIGH
SKELFFAL AND PLACENTA TISSUES AND AT V
HEART, LUNG AND BRAIN TISSUES.
-!- SIMILARITY: BELONGS TO THE SER/THR FAN
                                                                                                                                                                         -i- F
                                                                                                                                                                                               Schultz S.J., Nigg E.A.;
Schultz S.J., Nigg E.A.;
"Identification of 21 novel human protein kinases, including 3 members of a family related to the cell cycle regulator nimA of Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                Creasy C.L., Chernoff J.;
"Cloning and characterization of a
Ste20-like kinases.";
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                         SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STK3 OR MST2.
                                                                                                                                                                                                                                                         MEDLINE=94100173; PubMed=8274451;
                                                                                                                                                                                                                                                                                                                                                                                                      Gene 167:303-306(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96144292; PubMed=8566796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
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                                                                                                                                                        MAY PLAY A ROLE IN
                                            STE20 SUBFAMILY.
                                                                                                                                             SIMILARITY).
                                                                                                                                                                                     Growth Differ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VPSMSISASSQSSSVNSLADASDNEEEEEEEEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----EGHGEESSSEDSDIDGEAEDGEQGPIWTFPPTIRPSPHSKLHKG---TALHSSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQEAPNGPGAEAPEEEE----EAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VEACLNKDPRFRPTAKELLKHKFITRYTKKTSFLTELIDR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDSCLQKIPQDRPTSEVLLKHRFVLR-ERPPTVIMDLIQRTKDAVRELDNLQYRKMKKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KQSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKNNPPTLE-GHHSKPFKEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -PAEPIKRQPRSQCLSTLVRPVFGELKEKHKQSGGSVGALEELENAFSLAEESCPGISDK
                                                                                                                                                                                                                                                                                                    Natl. Acad.
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                                                                                                                                                                                     4:821-830(1993).
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                415
                                                                                                                                                        STRESS-ACTIVATED
                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                   93:10099-10104(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                        SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                  member
                                                                                                                                                                                                                                                                                                                             protein kinases,
                                                                                                                                                        SERINE/THREONINE KINASE ENVIRONMENTAL STRESS (BY
                                                                                    VERY
                                                                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                             ADP + a phosphoprotein
similarity).
                                                                                                LEVELS IN ADULT
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                                                        PROTEIN KINASES
                                                                                    LEVELS
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gh a collaboration EMBL outstation -
                                                                                    T KIDNEY,
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European Bioinformatics Institute.

There are no rest

no restrictions

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RESULT 5
ST24_HUMAN
ID ST24_H
AC Q9Y6E0
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DT 16-OCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
ST24_HUMAN STAN
Q9Y6EO; O14840;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U60206;
EMBL; Z25422;
HSSP; P24941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING
ACT_SITE
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkir
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:11406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00220; S_TKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase;
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                                                                                                  MIEHNSTMLESDLGTMVINSEDEEEEDGTMKRNATSPQ
                                                                                                                                                                                                            VDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELDNLQYRKMKKILF
                                                                                                                                                                                                                                              HSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAPANSFVGTPYWMAPEVILAMD 198
                                                                                                                                                                                                                                                                                                                                                                                                                        PEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQKL
                                                                                                                        EEEEEEEEE------EEEEEEEGPESREMAMMQ 405
                                                                                                                                                                       QEAPNGPGAEAPEEEEEAEPYMHRAGTLTSLESSHSVPSMSISASSQSSSVNSLADASDN
                                                                                                                                                                                                 VKKCLVKNPEQRATATQLLQHPFIKNAKPVSILRDLITEAMEIKAKRHDEQQRELEE---
                                                                                                                                                                                                                                                                       EGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRNF
                                                                                                                                                                                                                                                                                                HFMRKIHRDIKAGNILLNTEGHAKLADFGVAGQLTDTMAKRNTVIGTPFWMAPEVI----Q
                                                                                                                                                                                                                                                                                                                                                  DSPYVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKTLIEDEIATILKSTLKGLEYL
                                                                                                                                                                                                                                                                                                                                                                                                 PEEVFDVLEKLGEGSYGSVFKAIHKESGQVVAIKQVPV-----ESDLQEIIKEISIMQQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ase; Serine/threonine-protein kinase; ATP-binding.

27 278 PROTEIN KINASE
27 278 ATP (BY SIMILARITY).

56 56 56 ATP (BY SIMILARITY).

146 146 BY SIMILARITY).

146 146 BY SIMILARITY.

308 314 POLY-GLU.

96 98 WIV -> YLY (IN REF. 3).

121 121 D -> Y (IN REF. 3).

123 203 D -> E (IN REF. 3).

303 303 D -> E SY (IN REF. 2).

313 334 GEC -> ESY (IN REF. 2).

491 AA; 56261 MW; 9CA3B0644F3C14A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00107;
PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00107; PROTEIN_KINASE_ATP; 1.
PS00108; PROTEIN_KINASE_ST; FALSE_NEG
PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA80909.1;
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                                     STANDARD;
                                                                                                                                                  EEENSDEDEL
40, Created)
40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 595.5;
Pred. No. 9.8
                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                -DSHTMVKTSVGECGTMRATSTMSEGAQT
                                     443
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .8e-29;
                                     ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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Phosphorylation;
DOMAIN 36
NP_BIND 42
BINDING 65
BINDING 65
ACT_SITE 156
MOD_RES 18
VARSPLIC 1
                                                                                                                                 Pfam; PF00069; pkinase; 1.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                       EMBL; AF024636; AAB82560.
EMBL; AF083420; AAD42039.
HSSP; P24941; 1CKP.
Genew; HGNC:11403; STK24.
                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein
-!- COFACTOR: ISOFORM A REQUIRES MANGANESE FOR ITS ACTIVITY.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. -! - FUNCTION:
MUTAGEN
                                                                                                                                                                                                                    InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STE20-like kinase 3 that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of a human with unusual cofactor requirements.";
J. Biol. Chem. 272:28695-28703(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last annotation update) Serine/threonine protein kinase 24 (EC 2.7.1.37) (SMST3) (MST-3) (MSMMMBAIAN STE20-11ke protein kinase STK24 OR MST3 OR STK3.
                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pei G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20112812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=98019249; PubMed=9353338;
                                                                                                                       Fransferase;
                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schinkmann K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of a human brain-specific isoform of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE);
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ISOFORM A IS UBIQUITOUS. ISOFORM B J
EXPRESSED IN BRAIN WITH HIGH EXPRESSION IN HIPPOCAMPUS &
CEREBRAL CORTEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY PKA.
SIMILARITY: BELONGS
STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESIDUES.
                                                                                                                                                                                                                                                                             604984; -
                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T.-H., Ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTOPHOSPHORYLATED. ISOFORM B
                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long
                                                                                                                                                                                                                                                             IPR000719; Euk_pkinase
                                                                                                                    Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blenis J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275:2513-2519(2000).
PROTEIN KINASE THAT ACT ON BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Κ.,
                                                                                                            Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10644707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORM B), AND
                        286
50
65
156
18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is
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MDSRAQLWGLALNKRRATLPHPGGST
GMQ (IN ISOFORM A).
T->A: LOSS OF PHOSPHORYLATI
                                                   ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                          splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhou
                                       PHOSPHORYLATION (BY PKA)
                                                                                              PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SER/THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η.,
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OF PHOSPHORYLATION BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAMP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STE20-like protein kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASES
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                           v'
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                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                     s,
                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
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                           MAHSPVQSGLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
ST25_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   д
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                              "YSKI, a novel mammalian protein kinase structurally related to St and SPS1, but is not involved in the known MAPK pathways."; Oncogene 14:2047-2057(1997).

-i- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THE MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-i- ENZYME REGULATION: ACTIVATED BY PHOSPHOYRYLATION, PROBABLY AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHII THE KINASE ACTIVITY.

-i- SUBCELIQUAR LOCATION: Cytoplasmic.

-i- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED. HIGHEST LEVELS ARI FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND STOMACH FOLLOWED I
                                                                                                                                                                                                                                                                                                                                                                            ST225_HUMAN STANDARD; PRT; 426 AA.

000506; 015522;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant stress response kinase 1) (Ste20/oxidant stress response kinase-1) (SOX-1) (Ste20-like kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
SEQUENCE
            This
                                                                                                                                                                                               Ohno S.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=97042345; PubMed=8887545;
Pombo C.M., Bonventre J.V., Moinar A., Ky
"Activation of a human Ste20-like kinase
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                Osada S.-I., Izawa
                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-97304522; PubMed-9160885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                   SIMILARITY: BELONGS STE20 SUBFAMILY.
                                                        FOUND IN TESTIS, LARGE HEART AND LUNG.
 SWISS-PROT entry is copy
een the Swiss Institute
                                                                                                                                                                                                                                                             J. 15:4537-4546(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFL 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QKLRHPNTIQYRGCYLREHTAWLYMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAIKIIDL--EEAEDEIEDIQQEITVL
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49307 MW;
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           copyright.
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                                            THE SER/THR FAMILY OF
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Pred.
  of
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                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
ght. It is produced through Bioinformatics and the EN
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                                                                                                                                                                                                                Mizuno K.,
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No. 1.1e-28;
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                                             PROTEIN KINASES
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EMBL outstation
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         collaboration
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                                                                  ED BY
                                                                                                                                                          THAT
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Best Local
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                                                                                                            ZW.
                                                                                                                                   AMM
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RESULT 7

STIO_HUMAN STANDARD; PRT; 968 AA

ID ST10_HUMAN STANDARD; PRT; 968 AA

AC 094804; Q9UIW4;
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

E Serine/threonine-protein kinase 10 (EC 2.7.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation.
DOMAIN 20
NP_BIND 26
BINDING 49
ACT_SITE 140
CONFLICT 347
SEQUENCE 426 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; pD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SPROSITE; PS00100; PROTEIN_KINASE_ST; FALSE_NEG PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X99325; CAA67700.1; -. EMBL; D63780; BAA20420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000719; Euk_pkinase
InterPro; IPR002290; Ser_thr_pkir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 602255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:11404; STK25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF : | | : | | | : | : | : | : |
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                                                                                                                                                                                                                                                                                                                                                                        LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
                                                                                                                                                                                                                                                               -PAEPVKRQPRSQCLSTLVRPVFGELKEKHKQSGGSVGALEELENAFSLAEESCPGISDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                         406
                                                                                                                                                                                                                             404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270
34
49
140
348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.3%;
36.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
EP -> DA (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591; DB 1;
No. 1.5e-28;
   update)
2.7.1.37)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no rest
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(Lymphocyte-oriented

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                                                                                                                                  Query Match
                                                                                                                                                             ACT_SITE SEQUENCE
                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                      PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S.TKC; 1.
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002290; Ser_thr_pkir
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:11388; STK10.
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB015718; BAA35073.1;
EMBL; AL133081; CAB61400.1;
HSSP; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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Immunogenetics
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STK10 on Lo...
Homo sapiens (Human).
Mefazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STK10 OR LOK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=99216434; PubMed=10199912;
                                                                                                                                                                                                      NP_BIND
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
 88
                           83
                                                    31
                                                                               23
                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HISTONE IIA ON SERINE AND THREONINE RESIDUES (BY SIMILARITY). CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nitted (NOV-1999) to the EMBL/GenBank/DDBJ databases FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation
CDHPYIVKLLGAYYHDGKLWIMIEFCPGGAVDAIMLEL-DRGLTEPQIQVVCRQMLEALN 146
                         LRHPNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKPLQEVEIAAVTHGALQGLA 140
                                                    DPNEVWEIVGELGDGAFGKVYKA---KNKETGALAAAKVIETKSEEELEDYIVEIEILAT 87
                                                                 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                         al Similarity
125; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           н.,
                                                                                                                                                                                                                                                                                PS00107: PROTEIN_KINASE_ATP; 1.
PS00108: PROTEIN_KINASE_ST; 1.
PS50011: PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTOPHOSPHORYLATED (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                   IPR000719; Euk_pkinase
                                                                                                                                                           36
573
750
42
65
157
968 ;
                                                                                                         Conservative
                                                                                                                                                                                                                                                                  Serine/threonine-protein kinase; ATP-binding;
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49:369-375(1999).
                                                                                                                                                                                                                                                          Coiled
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884
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                                                                                                         65;
                                                                                                                      Score 515.5; DB 1;
Pred. No. 1.3e-23;
                                                                                                                                                                            ВУ
                                                                                                                                                                                    GLN-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                             COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                            PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                             SIMILARITY.
15E245193ECC553D CRC64;
                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kitamura F., Yonekawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no restrictions ng as its content is in
                                                                                                        145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gassenhuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the human,
                                                                                                                                  968;
                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
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RESULT 8
ST10_MOUSE
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055098;
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                             predominantly in lymphocytes.";

J. Biol. Chem. 272:22679-22684(1997).

-i- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN

HISTONE IIA ON SERINE AND THREONINE RESIDUES.

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a PISTONE SPECIFICITY: EXPRESSED PREDOMINANTLY IN

SUCH AS SPLEEN, THYMUS, AND BONE MARROW.
                                        ProDom; PD000001; Euk_pkinase; SMART; SM00220; S_TKc; 1.
                                                                                  MGD; MGI:1099439; Stk10.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
                                                                                                                                  EMBL; D89728; HSSP; P24941;
                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karasuyama H.;
"LOK is a novel mouse STE20-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STK10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein kinase 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40,
                                                                       Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kuramochi S., Moriguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97426413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                PTM: AUTOPHOSPHORYLATED.
SIMILARITY: BELONGS TO THE SER/THR FAMILY
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                                                                                                                                                 BAA24073.1;
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                                                                        pkinase;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase
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  (EC 2.7.1.37) (Lymphocyte-oriented
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N LYMPHOID ORGA
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PROSITE;

PS00107; PS00108;

PROTEIN\_KINASE\_ATP; 1.
PROTEIN\_KINASE\_ST; 1.
PROTEIN\_KINASE\_DOM; 1.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                       P35465; Q62934;
Ol-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated kinase 1) (PAK-1) (P68-PAK) (Alpha-PAK) (Protein kinase MUK2).
                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
MEDLINE=94150588; PubMed=8107774;
              TISSUE-Brain;
                                                                                                                                                                                         PAK1_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transterase;
                          SEQUENCE FROM N.A
                                                 NCBI_TaxID=10116;
                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                      567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                      ELRLLOKEEH 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRNFYDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRHPNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKPLQEVEIAAVTHGALQGLA 140
                                                                                                                                                                                                                                                                               EMAMMQEGEH 409
                                                                                                                                                                                                                                                                                                     LNKETGSLSLKGSKLHNKTLKRTRRFVVDGVEVSITTSKIISEDEKKDEEMRFLRRQELR
                                                                                                                                                                                                                                                                                                                                DNEEE--
                                                                                                                                                                                                                                                                                                                                                       NOSRPNSSALETLGGEALTNGGLELPSSYTPSHSKRASDCSNLSTSESMDYGTSLSADLS
                                                                                                                                                                                                                                                                                                                                                                                 EEAEPYMHRAGTL----
                                                                                                                                                                                                                                                                                                                                                                                                       LQTTSPADGLSKNDNDLKVPVPLRKSRPLSMDARIQMDEEKQIPDQDENPSPAASKSQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEDAVDAVPPLVNHTQDSANVTQPSLDSNKLLQDSSTPLPPSQPQEPVNGPCSQPSGDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DAVRELDN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRDFLKIALDKNPETRPSAAQLLQHPFVSRVTSNKALRELVAEAKAEVMEEIEDGREDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETMKDAPYDYKADIWSLGITLIEMAQIEPPHHELNPMRVLLKIAKSDPPTLLTPSKWSVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLHGKRIIHRDLKAGNVLMTLEGDIRLADFGVSAKNLKTLQKRDSFIGTPYWMAPEVVLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLHSHNMIHRDVKAGNILLSEPGLVKLGDFG----SASIMAPANSFVGTPYWMAPEVIL- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDHPYIVKLLGAYYYDGKLWIMIEFCPGGAVDAIMLEL-DRGLTEPQIQVVCRQMLEALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPNDVWEIVGELGDGAFGKVYKA---KNKETGALAAAKVIETKSEEELEDYIVEIEILAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine-protein kinase; ATP-binding; lon; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                         STANDARD;
                                                                                     (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
936
883
50
65
157
                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL).
GLN-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 511.5;
Pred. No. 2.
                                                            Craniata; Ver
Sciurognathi;
                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                              -TSLESSHSVPSMSISASSQSSSVN---SL-ADAS 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
7115EAC01032BF94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 160;
                                                                                                                                                                                         544
                                                                                                                                                                                                                                                                                                                                                                                                                                --LQYRKMKKILFQEAPNGPGAEAPEEE
                                                                          Vertebrata;
                                                                                                                                                                                         AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                             Muridae;
                                                                                                                                                                                                                                                                                                                              --EEEEEEEEEEEEEGPESR 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                             Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167;
                                                             Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                       506
                                                                                                                                                                                                                                                                                                                                                                                                                                332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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Query Match
Best Local S
Matches 117
                                                           Phosphorylation.
DOMAIN 75
DOMAIN 134
DOMAIN 269
NP_BIND 275
BINDING 298
ACT_SITE 388
                                              NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol.
                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extended the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTPASES TO THE JAK MAP KIMASE PATHWAY.

1: SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP
CDC42/P21 AND RAO1 (BY SIMILARITY).

1: TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BR
HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH
FUNCTION, AND AT LOVER LEYELS IN THE SPLEEN.

1: DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manser E., Leung T., Salihuddin H., Zhao Z.-S., Lim L.; "A brain serine/threonine protein kinase activated by Cdc42 and
                                                                                                                                                                                                       SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                         Pfam; PF00069; Pfam; PF00786;
                                                                                                                                                                                                                                                                                                                  EMBL; U49953; AAB615
PIR; S40482; S40482.
                                                                                                                                                                                                                                                                                                                            EMBL; U23443; AAB95646.1; -. EMBL; U49953; AAB61533.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 367:40-46(1994).
[2]
                                                                                                                                                                                                                               ProDom; PD000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 CRIB DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase (PAK) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Manser E., Chong C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96027610; PubMed=7559638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Racl."
                                                                                                                                               Transferase;
                                                                                                                                                         PROSITE;
                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        im L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY SIMILARITY: BELONGS TO THE SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIOL. Chem. 270:25070-25078(1995).
FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STE20 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXPRESSION ELSEWHERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
  117;
                                                                                                                                                                                                                                                                                                       P24941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.-I.,
             Similarity
                                                                                                                                                                   PS50108; CRIB; 1.
PS00107; PROTEIN_KINASE_ATP;
PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                         PS00108;
                                                                                                                                                                                                                                                   IPR000719; Euk_pkinase.
IPR000795; PAKbox/Rhobndng.
IPR002290; Ser_thr_pkinase.
0069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JAN-1998) to
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Izawa
                                                                                                                                            Serine/threonine-protein
                                                                                                                                                                                                                                                                                                        1CKP
                                                                                                                                                                                                                                           PBD;
                                                 AΑ;
                                                                                                                                                         PROTEIN_KINASE_ST;
                                                                                                                                                                                                                               Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Χ.
                                                            268
520
520
283
298
388
            23.6%;
                                                 60577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao Z.-S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a new member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ databases
                                                 MW;
 52;
Score 510; DB
Pred. No. 1.4e
52; Mismatches
                                                         LINKER.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽.
                                                                                                                       CRIB
                                               93BE32D8222F5B7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leung T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mizuno
                                                                                                                                            1.
n kinase;
                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ×.
            .4e
                      DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p21-Cdc42/Rac-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael G.,
                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suzuki A., Hirai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDC42/P21.
OF PROTEIN
                                                                                                                                            ATP-binding;
                      Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS WITH LITTLE
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                               restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDP-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BRAIN, WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hall C.,
                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                       Ø
14;
                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                           collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.-I.,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    no
6;
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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAK1_Huwan,
013153; Q13567;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated Serine/threonine-protein kinase PAK).
EMBL; U24152;
EMBL; U51120;
HSSP; P24941;
                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                  Curr. Biol. 7:202-210(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97199447; PubMed=9395435; Sells M.A., Knaus U.G., Bagrodia
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97199447; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                          between
                                                                                                                                                                                                                                                                                                       pathway.
                                                                                                                                                                                                                                                                                                                Brown J.L., Stowers L., Baer M., To
"Human Ste20 homologue hPAK1 links
                                                                                                                                                                                                                                                                                                                                          MEDLINE=96398842; PubMed=8805275;
                                                                                                                                                                                                                                                                                                                                                           TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human p21-activated kinase (Pak1) regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                                                                                 LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS GTPASES TO THE JNK MAP KINASE PATHWAY.
SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BI
                                                                                                           European Bioinformatics Institute.
                                                                                                                                                                                           SIMILARITY: BELONGS
                                                                                                                                                                SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                        CDC42/P21 AND RAC1.
                                                                                                                                                                                                                                                                          FUNCTION:
                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLNRCLEMDVEKRGSAKELLQHQFLKIAKPLSSLTPLIAAAKEATK 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQD11KEVRFLQK
                                                                                                                                                                                                                                                                                        Biol. 6:598-605(1996)
                                                                  non-profit institutions as long and this statement is not removed. requires a license agreement (See
                                                                                                                                                                                                         AUTOPHOSPHORYLATED WHEN ACTIVATED
                                                                                                                                                                               SUBFAMILY
  1CKP
                                                                                                                                                                                                                                                                         THE ACTIVATED KINASE ACTS
                            AAA65441.1; -.
               AAC50590.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                             TO
                                                                                                                                                                                           THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                           SER/THR
                                                                                                                                                                                                                                                                                                                Trejo J.,
iks GTPases
                                                                                                                                                                                                                                                                                                                                                                                                                                                       s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ambrose D.M.,
                                                                                                                                                                                          FAMILY
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S
                                                                                                                                                                                                                                                                          D
                                                                                                                                                                                                                                                                                                                Coughlin S. to the JNK
                                                                                                                                                                                                                                                            A VARIETY
                                                                               Usage
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                                                                                                                                                                                          OF PROTEIN
                                                                                                                                                                                                                                    BUT
                                                                                                                                                                                          PROTEIN KINASES
                                                                                                                                                                                                                                   NOT GDP-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                          organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bokoch
                                                                               bу
                                                                                                                                                                                                                                                            COF TARGETS
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                                                                                                                                                                                                                                                                                                                  MAP kinase
                                                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                     G.M.,
                                                                                                                        a collaboration -
                                                                                 for
                                                                                                                                                                                                                                                                                                                            J.;
                                                                                n no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495
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                                                                                                                                                                                                     RESULT 11
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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SMART; SM00220; S_TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN_
PROSITE; PS50011; PROTEIN_
                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MUTAGEN
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                           O88643;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK I (EC 2.7 kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK) (CDC4
SEQUENCE FROM N.A. MEDLINE=99282526; Burbelo P.D., Koza
                                                                                                   PAK-A)
                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                            NCBI_TaxID=10090
                                                                             Mus musculus (Mouse)
                                                                                         PAK1 OR PAKA.
                                                                                                                                                                               PAK1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation.
DOMAIN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkine
Pfam; PF00786; PBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew; HGNC:8590; PAK1.
MIM; 602590; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                                                                                                                                                                                                                                      LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                   FLNRCLDMDVEKRGSAKELLQHQFLKIAKPLSSLTPLIAAAKEATK
                                                                                                                                                                                                                                                         FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR
                                                                                                                                                                                                                                                                             TRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRD
                                                                                                                                                                                                                                                                                          DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN
                                                                                                                                                                                                                                                                                                                          LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                                                                                                                                                                                    NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALEF
                                                                                                                                                                                                                                                                                                                                                                                          LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY
                                                                                                                                                                                                                                                                                                                                                                                                             DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
117; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00107; PROTEIN_KINASE_ATP;
PS50011; PROTEIN_KINASE_DOM;
PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000719; Euk_pkinase.
IPR000095; PAKbox/Rhobndng.
IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    545
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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270
276
299
389
389
107
107
26
237
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                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pkinase;
             PubMed=10352232;
                                                         Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
269
521
521
284
299
389
379
379
   C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60661 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.5%;
  Finegold
                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY

L->F: CONSTITUTIVELY ACTIVE.

V-> A (IN REF. 2).

R-> L (IN REF. 2).

F-> S (IN REF. 2).

D-> E (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 508; I
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                                                     Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINKER
                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14A1E70E6480CD7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
  A.A.,
                                                                                                                                                                             545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase;
                                                                                                             EC 2.7.1.-)
(CDC42/RAC
                                                                 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
.8e-23;
  Hall A.,
                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         104;
                                                       Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 545;
  Pirone
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                             (p21-activated effector kinase
                                                                                                                                                                                                                                                          302
                                                                   Euteleostomi;
                                                         Murinae;
  D.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
                                                       Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                              496
                                                                                                                                                                                                                                                                                                                          436
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Query Match
Best Local
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BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1339975; Pakl.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00095; Pakbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
pfam; pr00069; pkinase; 1.
pfam; pr00786; PBD; 1.
Probom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00220; S_TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00285; PBD; SMART; SM00220; S_TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 232:209-215(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, central nervous the mouse PAK-1 and PAK-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00108; PROTEIN_KINASE_ST; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Cloning,
    497
                                                                                    437
                                           257
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                                                                                                                                                                                                               142
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                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                           23 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STE20 SUBFAMILY.
SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY). SIMILARITY: BELONGS TO THE SER/THR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED GTPASES TO THE JNK MAP KINASE PATHWAY (BY SIMILARITY). SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/F21 AND RAC1 (BY SIMILARITY).
                                                                                                                                                                                         LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                            LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY
FLQCCLEMDVEKRGSAKELLQHQFLKIAKPLSSLTPLMHAAKEATK
                                      FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR 302
                                                                                                         DEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN
                                                                                                                                                                 LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                                                                   NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALEF
                                                                                                                                                                                                                                                                                                                                   DPKKKYTPFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P24941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1CKP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88
267
521
521
284
299
389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               system expression and chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                   52;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 508; DB
Pred. No. 1.8e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRIB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A4861289534C3819 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
.8e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                     104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ЬУ
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                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                            141
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                                                                                 496
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Query Match
Best Local S
  Matches
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                                                                        Phosphorylation.
DOMAIN 70
DOMAIN 129
DOMAIN 268
NP_BIND 274
BINDING 297
                                                           DOMAIN
NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAK3_RAT STANDARD; PRT; 5
Q62829;
Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Serine/threonine protein kinase PAK 3
                                                                                                                                                                    SMART; SM00285; PBD; T.
SMART; SM00220; S.TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
-!- TISSUE SPECIFICITY: DETECTED AT HIGH LEVELS
LOW LEVELS IN THE TESTIS.
-!- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 270:25070-25078(1995).
1: FUNCTION: THE ACTIVARED KINASE ACTS ON A VARIETY OF TARGETS.
1: SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3 DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                         EMBL; U33314; AAC52268.1; -. HSSP; P24941; 1CKP.
                                                                                                                                                                                                                                                                                                                                             or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manser E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kinase 3) (PAK-3)
                                                                                                                                                 Fransferase;
                                                                                                                                                              PROSITE; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                   ProDom;
                                                                                                                                                                                                                                             Pfam; PF00786; PBD;
                                                                                                                                                                                                                                                                    InterPro; IPR000719;
InterPro; IPR000095;
InterPro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase (PAK) famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular cloning of a new member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-96027610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 CRIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STE20 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXPRESSION ELSEWHERE
al Similarity
116; Conserv
                                                                                                                                                                                                                                                           PF00069;
                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                  PD000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chong
 Conservative
                                                                                                                                                Serine/threonine-protein
                                                 AA;
                                                                                                                                                                                                                                                          pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    С.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rat).
                                                                                                                                                                                                                                  Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Beta-PAK) (P65-PAK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=7559638;
                                                                         83
267
519
282
297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND PARTIAL SEQUENCE OF
            23.4%;
                                                 60710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
                                                                                                                                                                                                                                                                                             Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao
                                                                                                                                                                                                                                                                   Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                  PAKbox/Rhobndng.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OT
                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z.-S., Leung
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE
                                                           PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
           Score 505; DB 1; Pred. No. 2.7e-23;
                                                                                                            LINKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SER/THR
                                                7B940FC204A2B48B CRC64;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update:
                                                                                                                                                            <u>.</u>.
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(EC 2.7
                                                                                                                                                kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBRYONIC CNS WITH LITTLE
                                                                                                                                                                      Τ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Michael G.,
 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae;
                                                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1.-) (p21-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDC42/P21.
OF PROTEIN KINASES
                                                                                                                                                ATP-binding;
                      Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN THE BRAIN AND
 Indels
                                                                                                                                                                                                                                                                                                                                                                    bγ
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                                                                                                                                                                                                                                                                                                                                                                                           restrictions
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14;
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Gaps
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Qy

14;

Gaps

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141 319 82

494 256 434 197 377

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RESULT 13
PAK3_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 3 (EC 2.7.
kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3).
                                                                                                                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                        This
                              SMART; SM00285;
                                                                   Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                         EMBL; AF068864; AAC36097.1; HSSP; P24941; 1CKP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=98400251; PubMed=9731525;
Allen K.M., Gleeson J.G., Bagrodia S., Partington M.W.,
Allen M.C., Cerione R.A., Mulley J.C., Walsh C.A.;

"PAK3 mutation in nonsyndromic X-linked mental retardation.";
Nat. Genet. 20:25-30(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                      InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00095; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                     Genew; HGNC:8592; PAK3
                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                          entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAK3 OR OPHN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAK3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN POSTMITOTIC NEURONS O
DEVELOPING AND POSTMATAL CEREBRAL CORTEX AND HIPPOCAMPUS.
PTM: AUTOPHOSPHORYLATED MHEN ACTIVATED BY CDC42/P21.
DISEASE: DEFECTS IN PAK3 ARE A CAUSE OF AN X-LINKED FORM OF
NONSYNDROMIC MENTAL RETARDATION (MRX30).
                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Bioinformatics Institute. There are no restricted the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
4
                                                                                                                                                                  300142; -
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                                                                                                                                                                                                                                                                     an
                                                   PD000001;
                                                                                                                                                                                                                                                                 non-profit institutions as long
and this statement is not removed.
requires a license agreement (See
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                              PBD;
                                               Euk_pkinase;
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                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
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PAK3_MOUSI
                            DЬ
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Best Local S
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                                         MEDLINE-99282526; PubMed-10352232;
Burbelo P.D., Kozak C.A., Finegold A.A., Hall
"Cloning, central nervous system expression an
the mouse PAK-1 and PAK-3 genes.";
Gene 232:209-215(1999)
                                                                                                                                                                                 Bagrodia
J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q61036; O88645;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
kinase 3) (PAK-3) (Beta-PAK) (CDC42/RAC effector kinase PAK-B).
PAK3 OR PAK-3 OR STK4 OR PAKB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
NP_BIND
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PROSITE;
PROSITE;
PROSITE;
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ACT_SITE
                                                                                                                                                                                                                                                               MEDLINE=96032693; PubMed=7559398;
Bagrodia S., Taylor S.J., Cresylor, C.L., Chernoff J., Cerione
"Identification of a mouse p21Cdc42/Rac activated kinase.";
J. Biol. Chem. 270:22731-22737(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).

Mus musculus (Mouse).

Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                          ERRATUM.
                                                                                                                                                                                                                                                                                                                                               TISSUE=Fibroblast;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAK3_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQNPERLSAVFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEYFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPKKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNL----QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FINRCLEMDVDRRGSAKELLQHPFLKLAKPLSSLTPLIIAAKEAIK 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS50108; CRLB; 1.
PS500107; PROTEIN_KINASE_ATP;
PS50011; PROTEIN_KINASE_DOM;
PS50011; PROTEIN_KINASE_ST;
                                                                                                                                                                                     S., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e; Serine/threonine-protein k
g; Phosphorylation.
g; Phosphorylation.
129 267 LINKER.
129 267 PROTEIN KI
268 519 PROTEIN KI
274 282 ATP (BY SI
297 297 ATP (BY SI
287 387 BY SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                   Taylor S.J., Creasy C.L., n. 271:1250-1250(1996).
                                                                                                                                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S_TKc; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                          ACTIVATED KINASE ACTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINKER.

PROTEIN KINASE.

PROTEIN (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 504; DB 1;
Pred. No. 3.1e-23;
2; Mismatches 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230AF6952CB049E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544
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                                                                                                                                                                                                       Chernoff
                          9
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                          A VARIETY OF
                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae;
                                                                                    chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 544;
                                                                                                      Pirone
                                                                                                                                                                                                       Cerione
                                                                                                                                                                                                                                                                                                          Cerione R.A.;
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R.A.;

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RESULT 15
SPS1_YEAST
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Best Local
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BINDING
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/orsend an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; pkinase; 1. Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000095; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF082297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U39738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SH3-binding; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           !ransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000001; Euk_pkinase;
                                                             495
                                                                                                                       435
                                                                                                                                                   198
                                                                                                                                                                                 378
                                                                                                                                                                                                              142
                                                                                                                                                                                                                                            320
                                                                                                                                                                                                                                                                                                        263
                                                                                                                                                                                                                                                                        83
                                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3 DOMAINS OF PHOSPHOLIPASE C-GAMA AND OF ADAPTER PROTEIN NCK. PTM: AUTOPHOSPHORLATED WHEN ACTIVATED BY CDC42/P21. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STE20 SUBFAMILY.
SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                                                                                                                               DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                          FLNRCLEMDVDRRGSAKELLQHPFLKLAKPLSSLTPLIIAAKEAIK
                                                                                                                TRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQNPERLSAVFHD
                                                                                                                                  DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEYFRN
                                                                                                                                                                                                                                        NKNPNIVNYLDSYLVGDELWVVMEYLAGGS--LTDVVTETCMDVGQIAAVCRECLQALDF
                                                                                                                                                                                                                                                                    LRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEV-EIAAVTHGALQGLAY 141
                                                                                                                                                                                                                                                                                                   DPKKKYTRLEKIGQGASGTVYTALDIATGQEVAIKQMNL---QQQPKKELIINEILVMRE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:1339656; Pak3
                                                                                      FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR
                                                                                                                                                                              LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                          LHSHNMTHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P24941; 1CKP
                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          70
129
268
274
297
297
387
161
161
361
493
493
525
544 AA;
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC52354.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC31969.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          267
519
282
282
297
387
161
493
525
                                                                                                                                                                                                                                                                                                                                                                                                                            60683 MW;
                                                                                                                                                                                                                                                                                                                                                                              23.1%;
                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKER.

LINKER.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

AT (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                             Score 500; L
                                                                                                                                                                                                                                                                                                                                                                                                                            C4AEB71DD33E6988 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              DВ
                                                                                                                                                                                                                                                                                                                                                                              .4e-23;
                                                                                                                                                                                                                                                                                                                                                                105;
                                                                                                                                                                                                                                                                                                                                                                                            Length 544;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                           540
                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                           197
                                                                                                                                                256
                                                                                                                                                                              434
                                                                                                                                                                                                                                         377
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ALD DOOR REPRESENTED DOOR REPRESENTED DOOR OF THE FIRST REPRESENTATION OF THE FIRST RE
      Matches
                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPS1_YEAST
P08458;
01-AUG-1988
                                                                                                                       NP_BIND
BINDING
ACT_SITE
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; Phouse...;
SMART; SM00220; S_TKC; 1.
SMO0220; S_TKC; 1.
SMO0220; PROTEIN_KINASE_ATP; 1
SMO0220; PROTEIN_KINASE_ST; FA
                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U13018; AAA64833.1; -. EMBL; U33057; AAB64963.1; -. EMBL; M13629; AAA35079.1; -. PIR; B25376; B25376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restitute the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENT.
-!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Friesen H., Lunz R.,
Submitted (AUG-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sporulation-specific protein 1 (EC SPS1 OR YDR523C OR D9719.27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                          Sporulation;
                                                                                                                                                                                                                                                                                                                                                                       Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed preferentially during sporulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percival-Smith A., Segall J.; "Characterization and mutatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 396-490 FROM N.A. MEDLINE=87064542; PubMed=3023934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S0002931; SPS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 6:2443-2451(1986)
                                  Similarity
                                                                                                                 469
490
      Conservative
                                                                                                                                                                                                                                            Meiosis.
18 272
24 32
47 47
                                                                                                                                                                                                                                                                                                                                                                Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE/THREONINE
                                                                                                                          ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55704 MW;
                               23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doyle
to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutational analysis of a cluster of three lly during sporulation of Saccharomyces
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                              314 KI-----LFQEAPNGPGAE-------APEEEEEAEPYMHRAGTLT-SLESSHSVPS 356
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Search completed: November 22, 2002, 12:24:17 Job time : 9.448 secs

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1: sp_archea:*
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3: sp_fung1:*
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6: sp_mammal:*
7: sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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646	677	902.5	987	1300	1480.5	1531.5	1537.5	1538.5	1540.5	1718.5	1726.5	1728.5	2133	2133	2161	Score	
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### ALIGNMENTS

DR DR DR	RP RA RL CC DR DR	RP RA	8 × 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT Q9JLS3 ID Q
1 20 2 2 2 3	SEQUENCE FROM N.A.  Chen Z., Hutchison M., Cobb M.;  Submitted (MAY 2000) to the EMBL/GenBank/DDBJ databases.  -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  EMBL, ARI40556; AAD39480.2;  EMBL, BAF140556; AAD39480.2;  INTERPROTEIN FROM 7.19; Euk_pkinase.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE=99428563; PubMed=10497253; Chen Z., Hutchison M., Cobb M.H.; "Isolation of the protein kinase TAO2 and identification of its miltogen-activated protein kinase/extracellular signal-regulated kinase kinase binding domain."; J. Biol. Chem. 274:28803-28807(1999).	TAC2. TAC2. Rattus norvegicus (Rat). Rattus norvegicus (Rat). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBL_TaxID-10116;	01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Serine/threonine protein kinase TAO2.	LT 1 S3 OJIS3 PRELIMINARY; PRT; 1235 AA.

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Best I
Yustein J.T., Robinson D., Templeton D.J., Kung I "Characterization of a Subfamily of Human STE20-; Selectively Activate p38 Through MKK3 and are Reg dependent Mechanism."; submitted (MAY-2000) to the EMBL/GenBank/DDBJ dati-; SIMILARITY: BELONGS TO THE SER/THR FAMILY OF EMBL; ARD20688; BAA74904.1; -. EMBL; AF263313; AAG38503.1; -. HSSP; P24941; 1B38.
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PROSITE; PS500110; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase SEQUENCE 1235 AA; 138750 MW; 426960D0812518AD CRC64;
                                                                                                                                          DNA
[2]
                                                                                                                                                   Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XII The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; DNA Res. 5:355-364(1998).
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                             SEQUENCE
                                                                                                                                                                                                                              MEDLINE=99156230;
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Q9UL54;
01-MAY-2000 (TrEMBLrel. 13, C:
01-MAY-2000 (TrEMBLrel. 20, L;
01-MAR-2002 (TrEMBLrel. 20, L;
Prostate derived STE20-like k
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PROSITE; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 1049 AA; 119280 MW; D6C5062F47794030 CRC64;
                                         organisation.";
J. Biol. Chem. 275:4311-4322(2000)
--- SIMILARITY: BELONGS TO THE SER
EMBL; AF061943; AAD45616.1; -.
HSSP; P24941; 1B38.
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                           activates
                                                                                                                                                                                                                      MEDLINE=20127920; PubMed=10660600; Moore T.M., Garg R., Johnson C., C
                                                                                                                                                                                                                                                                      SEQUENCE FROM
TISSUE=BREAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00069; pkinase; 1. PRINTS; PR00109; TYRKINASE.
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                                                                                                                                                  "PSK, a novel STE20-like kinase derived activates the JNK MAPK pathway and regul
                                                                                                                                                                                                      Morris J.D.H
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Ser_thr_pkinase.
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Best Local S
Matches 412
        Hutchison M., Berman K.S., Cobb M.H.;
"Isolation of TAO1, a protein kinase that activated protein kinase cascades,";
J. Biol. Chem. 273:28625-28532(1998).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMIL):
EMBL; AF084205; AAC71014.1; -.
EMBL; AF084205; AAC71014.1; -.
HSSP; P24941; 1B38.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
ProDom; pD000001; Euk_pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS050011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS050018; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protessequence 1235 AA; 138232 MW; 3AB9E8E690
                                                                                                                                                                                                                                                                                    O88664 PRELIMINARY; PRT; 1001 AA.
088664;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updatserine/threonine protein kinase TAO1.
                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                         MEDLINE=99003202; PubMed=9786855;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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Eutheria; Rodentia;
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PROTEIN_KINASE_ATP;
PROTEIN_KINASE_DOM;
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138232 MW; 3AB9E8E690934307 CRC64;
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                     InterPro; IPROC
InterPro; IPROC
Pfam; PF00069;
                                                                                                           Jenkins S.G., D'Andrea R.J., Gamble J.R., Vadas "Characterization of human TAOL.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ da-
-- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF EMBL; AB037782; BA492599.1;
EMBL; AV049015, AAL12217.1;
                                                                                                                                                                                                                                                                                                                      MEDLINE=20181126; PubMed=10718198;
Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.XVI
The complete sequences of 150 new cDNA clones from brain which code
for large proteins in vitro.";
DNA Res. 7:65-73(2000).
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ATP-binding; Kinase; Serine/threonine-g
SEQUENCE 1001 AA; 115952 MW; 85511F
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Mammalia; Eutheria;
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                                                                                          InterPro;
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                     IPRO0719; Euk_pkinase.
IPRO02290; Ser_thr_pkinase.
IPRO01245; Tyr_pkinase.
0069; pkinase; 1.
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    TYRKINASE
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Primates;
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115952 MW; 85511B62DBD62FCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
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Lest annotation (Fragment)
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2; Mismatches
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                                                                                                                                                                                                                                                   M.A.;
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Best Local S
Matches 330
PIAM: PF00069; pkinase; 1.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

SWART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                         dependent
Submitted
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09H2K7;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase;
NON_TER 1
                                                                                                                                                                                 Submitted (MAY-2000) to the EMBL/GenB
EMBL; AF263312; AAG38502.1; -.
HSSP; P24941; 1B38.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                InterPro; IPRO(
Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                Yustein J.T., Robinson D., Kung H.-J.; "Characterization of a Subfamily of Human Selectively Activate p38 Through MKK3 and
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STE20-like kinase (Fragment).
Homo sapiens (Human).
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79.3%;
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Pred. No. 8.6
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Matches 329
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MEDLINE=20384190; PubMed=10924369;

Zhang W., Chen T., Wan T., He L., Li N., Yuan Z.,

Zhang W., Chen T., Wan T., He L., Li N., Yuan Z.,

"Cloning of DPK, a novel dendritic cell-derived graduation of DPK, a
                                                                                                                                                                                                                                                            Submitted (FEB-2001) to the EMBL; AF13518; AAG99131.1; EMBL; BC002756; AAH02756.1; HSSP; P24941; 1B38.
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                                                                                                                                                                          MEDLINE-20162342; PubMed-10698516;
Yustein J.T., Li D., Robinson D., Kung H.J.;
"KFC, a Ste20-like kinase with mitogenic potent activate the SAPK/JNK pathway.";
Oncogene 19:710-718(2000).
EMBL; AF263314; AAF73045.1; -.
EMBL; AF263314; AAF73045.1; -.
HSSP; P24941; LB38.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Zn_MTpeptdse.
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
ATP-binding; Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFC (Fragment).
Gallus gallus (Chicken).
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01-OCT-2000 (TremBLrel.
01-MAR-2002 (TremBLrel.
                                                                                                           ProDom; PD000001; Euk_pkinase; SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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                                              PROSITE;
                                                                   PROSITE;
                                                                                                                                                            Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                          PS00107; PROTEIN_KINASE_ATP; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS00142; ZINC_PROTEASE; UNKNOWN
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  46E265937F218AA8 CRC64;
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annotation
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Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001230; Zn_MTpeptdse.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PRODOm; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00104; ZINC_PROTEASE; UNKNOWN_1.
ATP-binding; Kinase; Serine/threonine-protein
ATP-binding; Kinase; Serine/threonine-protein
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Best Local
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01-OCT-2000
01-MAR-2002
                                                                                                                                                                              Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. : - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL, AF181985; AAF25817.1; - HSSP; P24941; 1B38
                                                                                                                                                                                                                               Carter T.G., Benton B., Fruhling D., Monks C.R.F., Wind Kupfer A., Manfredi J., Johnson G.L., Plelaman C.M.; Kupfer A., Manfredi J., Johnson G.L., Plelaman C.M.; Winds and TAOl, two related proteins with kinase domain STE20, differentially relocate in mitogen stimulated T
                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NZM9;
                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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  SEQUENCE
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71.5%;
Serine/threonine-protein kii
105432 MW; 9738BD5DCFA12AC9
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15,
20,
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Pred. No. 2.5e
#3; Mismatches
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Query

Match

18

Score

1537.5;

В

4.

Length

Similarity

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RESULT
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       Query Match
Best Local S
Matches __291
                                                                                         InterPro; IPR000710; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00130; Zn_MTpeptdse.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PRODOm; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYrKC; 1.
PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00110; PROTEIN_KINASE_ST; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                           Kinase.
NON_TER
SEQUENCE
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Q1-MAR-2001 (TrEMBLrel. 16, C1

Q1-MAR-2001 (TrEMBLrel. 21, Lt

Q1-JUN-2002 (TrEMBLrel. 21, Lt

STE20-11ke kinase (Fragment).
                                                                                                                                                                                                                                                               dependent Mechanism.";
Submitted (MAY-2000) to the
EMBL; AF263311; AAG38501.1;
HSSP; P24941; 1B38.
                                                                                                                                                                                                                                                                                                                Yustein J.T., Robinson D., Kung H.-J.; "Characterization of a Subfamily of Human Selectively Activate p38 Through MKK3 and
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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THEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQE 121
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                     Similarity
                                                      898
Conservative
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                                                           ĀΑ;
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105501 MW;
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                   70.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation updat
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     Pred. No. 8.74
4; Mismatches
                               Score 1531.5;
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5; Mismatches
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                                                        E52C5BFEDD67264E CRC64;
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Best Local s
Matches 282
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OSUHG7;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TREMBLrel. 1
01-MAR-2002 (TREMBLrel. 2
                                                                             PRINTS; PRO0109; TYRKINASE.

PRODOM; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                           "Human JIK, a novel member of the STE20 kinase family that in JNK and is negatively regulated by epidermal growth factor."; J. Biol. Chem. 274:33287-33295(1999).
                                                                                                                                                                                                                                              -i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF EMBL; AF179867; AAF14559.1; -. HSSP; P24941; 1B38.
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STE20-like kinase
                                                                    ATP-binding;
                                                                                                                                                                            Pfam; PF00069; pkinase;
                                                                                                                                                                                      InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=20026851;
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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  Local Similarity
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                                                                                                                                                                                                                                                                                                                             0026851; PubMed=10559204; Biesova Z., Di Fiore P.P.,
                                                        868
  Conservative
                                                                   Kinase;
                                                      AA;
                                                        s; Serine/threonine-protein kinase; T
105657 MW; 61F04628713E6025 CRC64;
              68.5%;
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13,
20,
  48;
 Score 1480.5;
Pred. No. 7.6e
18; Mismatches
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Last annotation update)
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RX MEDLINE-20196006; PubMed=10731132;
RX MEDLINE-20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazed R.G., (Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazed R.G., (Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazed R.G., (Champe M., Pfeiffer B.D.,
RA Ballw R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Gherry J.M., Cawleys S., Dahlke C., Davenport L.B., Davies P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Glodek R., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeyamn C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
RA Nelson D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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01-MAY-2000 (Trem
01-MAR-2002 (Trem
CG14217 protein.
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Ephydroidea; Drosoph:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa; Arthropoda; Tracheata; He
Metazoa; Arthropoda; Diptera;
Neoptera; Endopterygota; Diptera;
a: Drosophilidae; Drosophila.
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O (TrEMBLrel.
2 (TrEMBLrel.
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13,
20,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393
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Q9NSW 10 O9NSW AC O9NSW DT 01-0C DT 01-0C DT 01-MA DE HYPOT GN DKFAR OC MARMA OX NCBI_RN [1]
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Best Local Similarity
                                                                                                Q9NSW2;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 118.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster.";
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ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0031030; CG14217.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
 SEQUENCE FROM N.A TISSUE=TESTIS;
                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                             Q9NSW2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003512; AAF48973.1; -. HSSP; P24941; 1B38.
                                                                                      Homo sapiens (Human).
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SEQUENCE 1039 AA; 1182
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                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                  SIS-ASSQSSSVNSLADASDN
                                                                                                                                                                                                                                                                                                                                                                                                     ESPALQSGHWSEYFRNEVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTGKQSQEKWQDILKEIRFLRQLNHPNTIEYKGCYLRESTAWLVMEYCVGSASDIIEVHK
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                                                                                                                                                                                                                                                                                                                             VRELDNLNYRKMKKILMVDTCETESAVGDTDDQQDD----HAGGDSSKSNSITSEHSIHSV
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                                                                                                                                                                                             PRELIMINARY;
                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.2%;
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Pred. No. 8.4e-92;
                                                         Craniata; Vo
Catarrhini;
                                                                                                                                                                                             PRT;
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                                                                       Vertebrata; Euteleostomi;
                                                          Hominidae;
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                                                                           Query Match
Best Local S
Matches 178
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Best Local S
Matches 194
                                                                                                                                                                                                                                                                                                                                                                                                                    Q9H755;
Q9H755;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
CDNA FLJ14314 fis, clone PLACE3000350, weakly similar serine/threonine-protein kinase SULU (EC 2.7.1.-).
Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
                                                                                                                                 Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM;

ATP-binding; Transferase.

SEQUENCE 398 AA; 46177 MW; BIADDII
                                                                                                                                                                                                                                                  Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Pujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Wiemann S
                                                                                                                                                                                                           InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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SEQUENCE 10
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ProDom; PD000001; Euk_pkinase; 1.
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EMBL; AL137701; CAB7(
HSSP; P02649; 1NFO.
                                                                                                                                                                                                                                                                                                                                                                   TISSUE-PLACENTA;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606
                                  177 APANSFYGTPYMMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYH 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SREMAMMQEGEHTVTSHSS: | | | | | | | | | | | | | | | | |
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                                                                              al Similarity
178; Conser
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nilarity 97.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Hypothetical protein; Transferase.
1062 AA; 118780 MW; A4B2B359EEC9CAAD CRC64;
à,
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                    T.,
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                                                                                          41.88;
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                                                                           Score 902.5;
Pred. No. 1.2e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 987; DB 4;
Pred. No. 1.3e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                    Bladdlda45d46FA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        398
                                                                                          1.2e-61;
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                                                                                                        DB 4;
                                                                             24;
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RESULT
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01-MAR-2001
01-MAR-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Physiol. 125:1342-1353(2001). EMBL; AY013245; AAG45491.1; -. HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Comparative sequence analysis of colinear artificial chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dubcovsky J., Ramakrishna W., SanMiguel P.J., Shiloff B.A., Bennetzen J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FNU3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
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                                                                                                                                                                                                      MSISASSQSSSVNSLPDVSDDKSELD---
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                                                                                      SEPGLVKLGDFGSAS----IMAPANSFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITC
                                                                                                                                                                                                                                                                        AVYKARDLRTQELVAIKIISLT--EGEEGYEDIRGEIEMLQQCSHPNVVRYFGSYQGEEY
                                                                                                                                                                                                                                                                                                                AVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHT 100
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IEMAEGMPPRSTVHPMRVIFMISSEPAPMLEDKEKWSLLFHDFIAKCLTKDPRLRPAASE
                                                                                                                                                                               LWIVMEYCGGGSVADLIGITEEPLDESQIAYICREALKGLAYLHSIFKVHRDIKGGNILL
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42 AA; 91646 MW;
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16,
20,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                          274
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Sear Job	Db	Qy	Db	Qy	Db	Qу	Db	Qy
Search completed: November 22, 2002, 12:26:18 Job time : 28.088 secs	678 TMPRHGN 684	410 TVTSHSS 416	618 INSETHDPKRAELISNEWAENTADIEANKEQYLDEHPDMQEAKTMPPSTGTVKKLKVAEG 677	368 VNSLADASDNEEEEEEEEEEEEEEEEEGPESREMAMMQEGEH 409	558 RINDDFGETVPTNPQQQTNHETYDGGAGDFGTMIVHPEDGDEVDESPIFPSSEFIPGLGS 617	329PEEEEEAEPYMHRAGTLTSLESSHSVPSMSISASSQSSS 367	509 MLKHKFIEKCNPGASKMLAKIKEAKKIRAKVAAETELSGPDSTMQDATV 557	DNLQ

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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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       2002, 12:21:31; Search time 9.152 Seconds
   US-09-060-410-4
US-09-060-410-17
US-09-060-410-17
US-09-060-410-17
US-09-111-709-8
US-09-111-228-8
US-09-393-569-2
US-09-319-340-993-5
US-09-152-406-3
US-09-152-406-3
US-09-153-40-93-1
US-09-151-930-4
US-09-151-930-4
US-09-151-930-1
US-09-151-930-3
US-09-151-930-3
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US-09-151-709-3
US-09-551-228-3
US-09-551-228-3
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Sequence 6, Appli	Sequence 3, Appli	Sequence 3, Appli	2,	Sequence 2, Appli	Sequence 19, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 5, Appli					

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US-09-060-410-4
                                                                                                                                      ; MOLECULE TYPE: protein US-09-060-410-4
                                                                                                                                                                   TELEFAX: (206) 004 ....4:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 993 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                  Query Match
Best Local Similarity
Matches 416; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application Patent No. 6165461
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                                                                                                                                                                                                                                                                                                                                                                             ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release #1.0, Vei

CURRENT APPLICATION UNMBER: US/09/060,410

FILING DATE: 14-APR-1998

CLASSIFICATION:
                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 8600
TELEPHONE: (206) 622-4900
TELEPHAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hutchinson, Michel APPLICANT: Chen, Zhu APPLICANT: Berman, Kevin TITLE OF INVENTION: TAO PROTITITE OF INVENTION: THEREFOR
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 6300 COCITY: Seattle STATE: Washing COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
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                                                                Score 2161; DB 4;
Pred. No. 2.1e-173;
; Mismatches 0;
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-060-410-2
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US-09-060-410-2
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GENERAL INFORMATION:
              Query Match
Best Local Similarity
                                                                                                                                                       TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 8600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622,4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino aci
                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: 14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                          TYPE: amino acid
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331;
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6300 Columbia Center, 701 Fifth Avenue
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                                                                                          linear
                                                                          protein
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              80.0%;
 32;
            Score 1728.5;
Pred. No. 5.16
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 Mismatches
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                             DB 4;
Indels
                             Length 1001;
21;
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US-09-060-410-17
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US-09-060-410-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17,
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: 14-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                              TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION UMBER: 31,392
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Berman, Kevin TITLE OF INVENTION: TAO ITITLE OF INVENTION: THERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Michele
APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 VRELDNLQYRKMKKLLFQEAHNGPAVEAQEEEEEQDHGGGRTGTVNSVGSNQSIPSMSIS
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                TOPOLOGY:
                              STRANDEDNESS:
                                                              LENGTH:
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                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09060410
                                                                                                                                                                                                                                                                                                                                                                                                                                           6300 Columbia Center,
                                                                278 amino acids
                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEED and BERRY LLP
                                                                                         ) 682-6031
NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAO PROTEIN KINASES AND METHODS THEREFOR
                                                                                                                                                                860098.421
                                                                                                                                                                                                                                                                                                                                                                                                                                           701 Fifth Avenue
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Query Match

40.48;

Score 873.5;

DB 4;

Length 278;

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US-08-712-709-8
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                                                   Query Match
Best Local Similarity
Matches 147; Conserv
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APPLICANT: Au-You
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/7: FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
                                                                                                                                                                                                                                              MOLECULE TYPE: F
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                      1MEDIA: GE...
LIBRARY: GE...
1117791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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10 LKDPDVAELFFKDD-----PEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSG 63
                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPAL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNEKWODIIKEVRFLOKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQE 125
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                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                               single
  28.0%; SCULT 34.0%; Pred. No. 5.50 160; rive 70; Mismatches 160;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip
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                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111
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MEDIUM TYPE: Diskett
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APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
                                                                                                       SEQUENCE CHARACTERISTICS
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STREET: 51,
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                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQEVEIAAVTHGALQGLAYLHSHNMTHRDVKAGNILLSEPGLVKLGDFGSA----SIMAP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KDAVRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRA---------
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                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09541228

Patent No. 6232077

GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
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IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1117791
ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J
                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                          SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
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                                       FILING DATE:
                                                                                       FILING DATE:
                                                                                                                                                            COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                        CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                             STREET:
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ses 147; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ESDLQEIIKEISIMQQCDSPHVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKT 120
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                                                                                                                                                                                                                                      94304
                                                                                                                                                                                                                                                                          CA
                                                                                                                                                                                                                                                                                                           3174 Porter Drive
                                                                                                                                                                                                                                                       U.S.
                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                            Incyte Pharmaceuticals,
                                                                                                                                                                                                   Diskette
                                                                                                                                                                DOS
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                                                                                                           US/09/541,228
                                                       08/712,709
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GENERAL INFORMATION:
APPLICANT: BINGHAM, SHARON
APPLICANT: CASE, PATRICK
APPLICANT: LAWSON, SALLY NEALE
APPLICANT: LAWSON, RICHARD ANTHONY
APPLICANT: PIERCY, VALERIE
APPLICANT: RAUSCH, OLIVER LARS
APPLICANT: RAUSCH, OLIVER LARS
APPLICANT: RAVAL, PRAVIN
APPLICANT: SANGER, GARETH JOHN
APPLICANT: SANGER, GARETH JOHN
APPLICANT: SANGER, GARETH JOHN
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US-09-393-569-2
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
SEQUENCE 487 amino acids
FILE REFERENCE: P32261
CURRENT APPLICATION NUMBER: US/09/393,569
CURRENT FILING DATE: 1999-09-10
EARLIER APPLICATION NUMBER: GB 9907261.3
                                                                                        TITLE OF INVENTION: NEW USE
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REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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TOPOLOGY: lin
MOLECULE TYPE:
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LIBRARY: GenBank
CLONE: 1117791
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Pred. No. 5.5e-43;
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FILE REFERENCE: PHM.70296

CURRENT APPLICATION NUMBER: US/09/211,930

CURRENT FILING DATE: 1998-12-15

EARLIER APPLICATION NUMBER: GB 9726851.0

EARLIER FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FRASTSEQ FOR Windows Version 3.0

SEQ ID NO 5

LENGTH: 431

TYPE: PRT

ORGANISM: Homo Sapiens

US-09-211-930-5
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US-09-211-930-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09211930
Patent No. 5962265
GEMERAL INFORMATION:
APPLICANT: Tyrell E. No. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: SERING/THREONINE KINASE
FILE ENERGENCE AND ASSESSED OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 1360
TYPE: PRT
Query Match
Best Local Similarity
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EARLIER APPLICATION NUMBER: GB 9819779.1
EARLIER FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 5
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Pred.
594; DB 2;
No. 4.3e-42;
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RESULT 10
US-09-152-406-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 431
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Best Local Similarity
Matches 130; Conserv
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REFERENCE: PHM. 70296.N1
CURRENT APPLICATION NUMBER: US/09/340,993
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930
EARLIER FILING DATE: 1997-12-19 & 1998-12-15
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                                                                                                                       256 NFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPT-VIMDLIQRTK 298
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                                                                                                                                                                                                                                                                                      AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                                                                                                                                                                        KADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAIKIIDL--EEAEDEIEDIQQEITVL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
                                                                                                                                                                                  --KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE-GNYSKPLK 248
                                                                                                                                                                                                                                                             DYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI-
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                                                                                                    EFVEACLNKEPSFRPTAKELLKHKFILRNAKKTSYLTELIDRYK
                                                                                                                                                                                                                     AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFR
                                                                                                                                                                                                                                                                                                                                               SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL
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o. 6034228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.5%; Score 594; DB 3;
45.8%; Pred. No. 4.3e-42;
ative 48; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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6265560

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GENERAL INFORMATION:
APPLICANT: William Craig Moore
APPLICANT: Tyrell E. No. 6265560ris
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN STE20-LIKE STRESS ACT
TITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM. 70272
CURRENT APPLICATION NUMBER: US/09/152,406
CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION UNMBER: 9719920.2
EARLIER APPLICATION UNMBER: 9719920.2
EARLIER FILING DATE: 1997-09-19
NUMBER OF SEO ID NOS: 9
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US-09-468-442-5
; Sequence 5, Application US/09468442
; Patent No. 630098
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CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/340,993
EARLIER FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER APPLICATION NUMBER: US 09/211,930
EARLIER APPLICATION NUMBER: US 09/211,930
EARLIER APPLICATION NUMBER: US 09/211,930
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Best Local S
Matches 130
                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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SEQ ID NO 3
LENGTH: 431
TYPE: PRT
ORGANISM: Homo Sapiens
  Best Local Similarity
                       Query Match
                                                                  LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
-09-468-442-5
                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE FILE REFERENCE: PHM.70296.N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tyrell E. No. 6300098ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 DYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI- 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 KDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVÄIKKMSYSGKQSNEKWQDIIKEVRFL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL 132
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45.8%; Pred. No. 4.3e-42;
45.8%; o. mismatches 92;
  27
45.
  Score 594; DB 4; Pred. No. 4.3e-42;
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US-08-852-743-2
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Query Match
Best Local Similarity
Matches 154; Conserv
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                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                    MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/016,774
FILING DATE: 7-MAY-1996
ATTORNEY_AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786,
                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                          TELEFAX: U.T. 200154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 NFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPT-VIMDLIQRTK 298
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                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 7
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/852,743 FILING DATE: 7-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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27.4%; ilarity 36.4%; Conservative 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Force, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                   linear
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                                                                                    protein
internal
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SOK-1 AND
   69;
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Score 592; DB 2; Length 426; Pred. No. 6.2e-42; 9; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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 72;
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Gaps
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Sequence 4, Application US/09211930

Patent No. 5962265:
GENERAL INFORMATION:
APPLICANT: Tyrell E. No. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM. 70296

CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT FILING DATE: 1998-12-15
CURRENT FILING DATE: 1998-12-15
COURTER APPLICATION NUMBER: US/09/211,930
                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 426
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-211-930-4
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                LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 197
                                                                                                                                  DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ 72
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LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
                                                                   CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK -- PGPLEETYIATILREILKGLDY
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                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                          27.4%; Score 592; DB 2; Length 426; 36.4%; Pred. No. 6.2e-42;
                                                                                                                                                                                                         69; Mismatches 128;
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CURRENT APPLICATION NUMBER: US/09/340,993
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930
EARLIER FILING DATE: 1997-12-19 & 1998-12-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 27.4%; Score 592; DB 3; Length 426; Best Local Similarity 36.4%; Pred. No. 6.2e-42; Matches 154; Conservative 69; Mismatches 128; Indels
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APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
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ORGANISM: Homo sapiens
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VPSMSISASSQSSSVNSLADASDNEEEEEEEEE-----EEEEEE-----EEEEGPESREM 401
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                                                                                                                               VEACLNKDPRERPTAKELLKHKFITRYTKKTSFLTELIDR-----YKRWKS--
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; FRAGMENT TYPE:
US-09-185-370-2
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US-09-185-370-2
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                         Best Local Similarity Matches 154; Conserv
                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pombo, Celia M.
APPLICANT: Bonventre, Joseph
TITLE OF INVENTION: SOK-1 AND METHODS
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NUMBER OF SEQUENCES:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                 LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 197
                                                                                                                               CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY 130
                                                                                                                                                                                        DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EBAEDEIEDIQQEITVLSQ 72
                                                               LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI--- 187
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                                                                                                                                                                                                                                                         69;
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                                                                                                                                                                                                                                                      Score 592; DB 3;
Pred. No. 6.2e-42;
9; Mismatches 128
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                                                                                                                                                                                                                                                                                     Length 426;
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                           402 AMM 404
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                                                                                                            ----EGHGEESSSEDSDIDGEAEDGEQGPIWTFPPTIRPSPHSKLHKG---TALHSSQK 344
                                                                                                                                      -EEEEE-----EEEGPESREM 401
                                                                                                                                                                   ----YKRWKS--
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Search completed: November 22, 2002, 12:28:06 Job time: 11.402 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002, 12:18:00 ; Search time 25.376 Seconds (without alignments) 2184.436 Million cell updates/sec
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              Human/Murine SULU3
Novel human protei
Murine SULU3 prote
Human ORFX ORF2955
                                                                                                                                                                                      Description
                                                                                 Human kinase (PKIN Human KDS2 protein Rat TAO1 kinase.
                                                                                                                                   Rat TAO2 kinase.
Human ORFX ORF1427
                                                                                                                                                                                                                                                                                       to have a
being printed,
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Novel human diagno	ABG04990	22	458	26.9	581
ein SEQ	AAM78421	22	1339	7.	585.5
phila m		22	596	7.	587
acid s	AAY68771	21	431	7.	588
n STE20	AAY55949	20	426	7.	591
e C12.	AAY21672	20	413	27.3	591
MAPK-	AAY82275	21	426	7.	592
-N-kinase pr	AA020953	23	443	7.	594
Ste20-like	AAY82276	21	431	7.	594
STE20-like	AAY04473	20	431	7.	594
Human MST3 protein	AAY55950	20	431	7.	594
ypept	AAB97069	22	431	7.	596
prot	AAW31603	18	426	7.	601
NIK-Rela	AAB50059	22	1360	8	605
prote	AAY85263	21	1360	8	605
acid	AAB68219	22	1353	8	605
acid	AAB68217	22	1332	8	605
acid	AAB68221	22	1324	8	605
acid	AAB68218	22	1306	œ •	605
acid	AAB68222	22	1298	8	605
acid	AAB68220	22	1277	8	605
acid	AAB68223	22	1269	œ	605
protei	AAM79405	22	1385	28.0	606
_	AAY21674	20	487	8	614.5
protei	AAM25383	22	163	0	660
	AAY55937	20	786	2	692.5
protein seq	AAB95890	22	398	1	20
X ORF58	AAB40294	21	1062	5	987
tode STE2	AAY55955	20	982	7.	1032.5
signal t	AAU17256	22	265		1119
centr		22	265	51.8	1119
ophila melano	911	22	1039	0	1300
central ner	8711	22	323	۳.	320
SULU1 prote	559	20	898	70.9	1531.5
Human cell signall	AAY44244	21	898	70.9	532

### ALIGNMENTS

RESULT 1 AAY49897

AAY49897 standard; Protein; 993

AA

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TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder;
                  N-PSDB;
                           WPI; 1999-633831/54.
                                                                                                 14-APR-1999;
                                                                                                                                                     Rattus sp.
New polypeptides that phosphorylate kinase, used to screen
                                                             (TEXA )
                                                                               14-APR-1998;
                                                                                                                   21-OCT-1999.
                                                                                                                                     W09953076-A1
                                                                                                                                                                        neurodegeneration; MAP kinase;
                                                                                                                                                                                                                     Rat TAO2 kinase.
                                                                                                                                                                                                                                       27-JAN-2000
                                                             UNIV TEXAS SYSTEM
                                           Hutchison M,
                                                                                                                                                                                                                                       (first
                                                                               98US-0060410
                                                                                                 99WO-US08165
                                                                                                                                                                                                                                       entry)
                                            Chen
                                            2,
                                                                                                                                                                        MAP/ERK kinase
                                             Berman
for
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AAW97676

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ARBSULT 2
AAB4168
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XX BE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents rat TAO2 protein kinase, which is capable of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related polypeptides, are used to screen for modulators of stress-responsive mitogen activated protein (MAP) kinase pathways. These modulators are potentially useful for treating or preventing: (1) inflammation, and uncommune disease, cancer and degeneration (inhibitors of phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders and neurodegeneration (enhancers of phosphorylation). TAO kinases are also used to raise specific antibodies, useful therapeutically as modulators and as immunoassay reagents for detecting TAO kinases.

TAO kinase polynucleotides can be used: (a) for recombinant expression of TAO kinases; and (b) in the form of fragments, for detecting TAO kinases are highly specific for MEK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                 antianaemic; gene therapy; cancer; proliferative disorder; hypertoneurodegenerative disorder; osteoarthritis; graft vs host disease,
                                                 vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopath; antiarthritic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antialidabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
   cardiovascular
                                                                                                                                                                                    Human ORFX ORF1427 polypeptide sequence
                                                                                                                                                                                                                                                                                                   AAB41663 standard;
                                                                                                                                                                                                                            08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                                                                                                                                                                                                                                                                                                                                                                                                               ASSOSSSVNSLADASDNEEEEEEEEEEEEEEEEEEGPESREMAMMQEGEHTVTSHSS
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                                                                                                                                                 reading
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                                                                                                                                                                                                                                                                                                   Protein; 1235
                                                                                                                                               frame; ORFX; detection;
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e). TAO kinases, and related
hypothyroidism;
                                                                                                                                             cytostatic; hepatotropic;
                                                                                                                                                                                      NO:2854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                    hypertension;
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KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN

180 120

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YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK

SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN

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                                           B
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                                                                                                                                                                                                                antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; cosqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allocations and present allocation disorders, asthma, burner is considered.
                                                                                                                                                Query Match
Best Local
                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                   allergies, aplastic anaemia, burns, wounds, bone and cartilage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholesterol ester storage; systemic lupus erythematosus; infection, severe combined immunodeficiency; malaria; autoimmune disorder; ast allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets RA,
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  61
                                                                                                                                                  Local Similarity
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                                                             1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
  YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                           MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
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)B; AAC75872.
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                                                                                                                                                                                                             1235 AA;
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                98.7%;
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Pred.
                                                                                                                               Mismatches
                                                                                                                                                2133; DB 21;
No. 1.4e-172;
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RESULT 3
AAE04366
ID AAE0
XX AAE0
AX AAE0
AX AAE0
AX AAE0
AX AAE0
AX Huma
XX Huma
XX Huma
XX Hom
KW 11pi
KW 2gene
KW anti
KW 2gene
KW anti
KW 7gene
KW anti
KW PFT Dome
FFT Dome
FFT Reg
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  Claim
                                                   Novel human kinase proteins (PKIN) useful for diagnosing, preventing immune disorders, cardiovascular diseases and affecting growth and development associated with abnormal PKIN -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipid disorder; cancer; fatty liver; cholestasis; transgenic animal; gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological; antidiabetic; nephrotophic; antiulcer; antiarthritic; antirheumatic; antipsoriatic; neuroprotective; cytostatic; hepatotrophic; osteopathic; vasotropic; antianginal; anorectic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kinase; PKIN-7; therapy; immune disorder; Addison's disease; AIDS; acquired immune deficiency syndrome; growth and developmental disorder; arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma; leukaemia; cardiovascular disease; myocardial infarction; hypertension;
                                                                                                                                                                                                                                                        Yang
                                                                                                                                                                                                                                                                                                                                                       21-JAN-2000;
28-JAN-2000;
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14-JAN-2000;
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                                                                                                                                                                                                                                  , MC,
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1;
                                                                                                                                                                   AAD08640
                                                                                                                                                                                                                                                                                                         INCYTE GENOMICS INC
Page 111-113;
                                                                                                                                                                                                                                  Baughn MR,
Lal P, Kha
                                                                                                                                                                                                                                                                                                                                                     ; 99US-0172066.
; 2000US-0176107.
; 2000US-0177731.
; 2000US-0178573.
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128pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Protein
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RESULT 4
AAW97677
ID AAW9
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AC AAW9
XX DT 10-W
XX Huma
XX KDS2
KW KDS2
KW Lhre
XX Homc
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XX Homc
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful to detect upstream sequences such as promoters and regulatory elements, for creating knock in or knock out in humanised animals or transgenic animals to model human disease and for somatic or germline gene therapy for treating the above mentioned disorders. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and myelofibrosis; cancers such as adenocarcinoma and leukaemia, cardiovascular diseases such as myocardial infarction and hypertension, and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune haemolytic anaemia, autoimmune thyroiditis, multiple sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis and diabetes mellitus; growth and developmental disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel human kinase proteins (PKIN) and nucleic acid molecules encoding them. PKIN is useful for identifying compounds that modulates its activity. PKIN cDNA is useful for assessing toxicity of a test compound. PKIN and its cDNA are useful for diagnosis, prevention and treatment of immune disorders such as acquired immune deficiency syndrome (AIDS), Addison's disease, anaen adult respiratory distress syndrome, allergies, amyloidosis, psoriae adult respiratory distress syndrome, allergies, amyloidosis, psoriae
                                                                                                                              Human
                                                                                                                                                                                                                                       AAW97677 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                    Homo sapiens
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                                                                                                                              KDS2
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                                                                      kinase;
                                                                                                                          protein kinase
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                                                                    domain related to Ste20; human; serine nase; protein kinase; signal transduction
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Pred. No. 2.5e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein associated with signal transduction. KDS2 has a Ck kinase domain related to that of Ste20 (KDS1 = Kinase Domain CC related to Ste20). KDS2 cDNA (see AAX07075) was isolated from a CC human bone marrow cDNA library. A clone (see AAX07074) encoding the highly homologous KDS1 (see AAW97676) was also obtained. Both KDS1 cand KDS2 have Glu/Gln-rich regions at their C-terminus (see also CC AAW97678-79) suggesting an alpha-helical structure that may play a crole in covalently localising these proteins to a specific site within the cells, which may be necessary for function. A method CC within the cells, which may be necessary for successed such as since CC within the cells, which may be necessary for successed such as since CC within the cells, which may be necessary for successed such as signal CC transduction pathways. These pathways may regulate cytoskeleton, can secretion, growth, apoptosis, superoxide generation, and specific contents of the company of the compa
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 31; Page 85-88; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated vertebrate kinase - used to develop products for the diagnosis and treatment of disorders involving cellular processes such as signal transduction processes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription. KDS polypeptides and polynucleotides can for treating disorders involving aberrant expression of alian KDS genes. They can also be used for detection,
                              ASSQSSSVNSLADASDN--EEEEEEEEEEEEEEEGPEAREMAMMQEGEHTVTSHSS
                                                                                                                                                 VRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEEAEPYMHRAGTLTSLESSHSVPSMSIS
                                                                                                                                                                                                                                                   ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLKERPPTVIMDLIQRTKDA
                                                                                                                                                                                                                                                                                                                                                                                                                    KPLQEVEIAAVTHGAVQGLAYLQSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YSGKQSNEKWQDIIKEVRFLQKVRHPNTIQYRGCYLREQTAWLVMEYCLGSAFDLLEVHK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                                                        ASSQSSSVNSLADASDNEEEEEEEEEEEEEEEEEEEGPESREMAMMQEGEHTVTSHSS 416
                                                                                                                        VRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRAGTLTSLESSHSVPSMSIS
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1 drug sc
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97.6%;
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Pred. No. 6.6e-170;
3; Mismatches 5;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                     phosphorylation); or (2) insulin resistant diabetes, metabolic disorded and neurodegeneration (enhancers of phosphorylation). TAO kinases are also used to raise specific antibodies, useful therapeutically as modulators and as immunoassay reagents for detecting TAO kinases. TAO kinases polynucleotides can be used: (a) for recombinant expression of TAO kinases; and (b) in the form of fragments, for detecting TAO kinases; and (b) in the form of fragments, for detecting TAO kinases; and (b) in the form of fragments, for detecting TAO kinase polynucleotides in standard hybridisation and amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents rat TAO1 protein kinase, which is cape of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related polypeptides, are used to screen for modulators of stress-responsive mitogen activated protein (MAP) kinase pathways. These modulators are potentially useful for treating or preventing: (1) inflammation, autoimmune disease, cancer and degeneration (inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder; neurodegeneration; MAP kinase; MAP/ERK kinase.
                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                     kinase polynucleotides in standard hybr
tests. TAO kinases are highly specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 1; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptides that phosphorylate kinase, used to \operatorname{modulators} for treating e.g. cancer or inflammation
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181 SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN 240
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                                                                                                                                                                                                              1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS 60
                                                       KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN 180
                                   KPLQEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN 180
                                                                                                                                          YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                                                                                                                                                             MPSTNRAGSLKDPEIAELFFKEDPEKLFTDLREIGHGSFGAVYFARDVRTNEVVAIKKMS 60
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                                                                                                       YSGKQSTEKWQDIIKEVKFLQRIKHPNSIEYKGCYLREHTAWLVMEYCLGSASDLLEVHK 120
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                                                                                                                                                                                                                                                                                                                         1001 AA;
                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                  80.0%;
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Pred. No. 2.9e
32; Mismatches
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                                                                                                                                                                                                                                                 .9e-138;
es 32;
                                                                                                                                                                                                                                                                                    DB 20;
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                                                                                                                                                                                                                                                                                  Length 1001;
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RRESULT 6
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XX AAY5942
XX AAY5942
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XX AAY5
DE Huma
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This sequence represents a consensus peptide sequence conained in novel STE20-related protein kinases. The invention relates to a nucleic acid molecule encoding a kinase polypeptide selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic; vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK6; STLK7 ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist; antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma; inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis; rhinitis; autoimmunity; organ transplantation; multiple sclerosis; rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oxidative stress-related neurodegenerative disorder; Parkinson's disease; amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel kinase-related polypeptides used for the diagnosis and treatment of kinase-related diseases and disorders \,
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                                                                                                                                                                                                                                                                                                                                                                 Page 312-315; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Martinez
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                                                                                                                                                                                               Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene t neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                ABB97326 standard; Protein;
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                                         11-SEP-2000;
                                                                                                  21-MAR-2002.
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             (HYSE-) HYSEQ INC
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Matches 330
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                                  neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabout vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK5
                                                                                                                                    Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic; antipsoriatic; antiatteriosclerotic; antiasthmatic; immunosupressive;
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DB; ABN32512.
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79.3%;
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I, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                           748
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Pred. No. 4.3e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao
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                                                          antagonist;
                                                                                                            antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren
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KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN 180

KPLQEVETAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN

SFYGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN

240 180

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SFYGTPYWMAPEVILAMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN

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                                                                                                                                                                                                                                              cc invention relates to nucleic acid molecule encoding a kinase polypeptide cselected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, CC24, KHS2, STLU1, SULU3, GEKZ, PAK4 and PAK5. The proteins are used to cc identify agonists and antagonists, and to raise antibodies. The collectides are useful in gene therapy protocols. The polypucleotides, antibodies, antagonists and agonists may be used to treat clientees such as immune-related disorders and diseases (e.g. rheumatoid arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g. ccoln's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, cronic inflammatory bowel disease (e.g. crinitis, autoimmunity, and organ transplantation, chronic inflammatory clientees (e.g. crinitis, autoimmunity, and organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative cstress-related neurodegenerative disorders (e.g. amylotrophic lateral cc stress-related neurodegenerative disorders (e.g. amylotrophic lateral cc sclerosis, parkinson's disease and Leigh syndrome), cancer, cardiovascular disorders, inflammatory disorders, diabetes cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes cuseful for cell growth regulation (e.g. in wound healing), T cell cardiovation, mitosis control, and as immunosuppressants
                                                                                                                                                                 Matches
                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel kinase-related polypeptides used for the diagnosis and treatment of kinase-related diseases and disorders \,\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxidative stress-related neurodegenerative disorder; Parkinson's disease amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; ischemic disorder; inflammation; diabetes mellitus; fibrosis; microsis; mesangial disorder; growth regulation; wound healing; T cell activation;
                                                                                                                                                                                                                                                                                    activation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plowman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1999
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                                       YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                                                             MPSTNRAGSLKDPEIAELFFKEDPEKLFTDLREIGHGSFGAVYFARDVRTNEVVAIKKMS
                                                                                                                       MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
  YSGKQSTEKWQDIIKEVKFLQRIKHPNSIEYKGCYLREHTAWLVMEYCLGSASDLLEVHK
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                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                    mitosis
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a novel STE20-related protein kinase.
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                                                                                                                                                                                                                                                                                  control,
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77.9%;
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                                                                                                                                                               32;
                                                                                                                                                             Score 1670.5; I
Pred. No. 1.7e-J
2; Mismatches
                                                                                                                                                                                                                                                                                  and as immunosuppressants
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                                                                                                                                                                                                  DB 20;
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                                                                                                                                                               29;
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RESULT 9
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames I to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; lmmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                              Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anticonvulsant; osteopathic; antiarthritic; immunosuppressant; ca
immunostimulant; thrombolytic; coagulant; vasotropic; antidiabeti
hypotensive; dermatological; immunosuppressive; antiinflammatory;
antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
N-PSDB; AAC77400.
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                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000WO-US08621.
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                                                                                                                                                                 Page 5088-5090; 5507pp; English
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99US-0127636.
99US-0127728.
2000US-0540763.
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                                                                                                                                                                                                                                                                                                                     Leach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nootropic; neuroprotective;
immunosuppressant; cardiant;
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RESULT 10
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                     08-JUL-1997;
                                                                                             21-JAN-1999
                                                                                                                                                                              threonine kinase;
                                                                                                                                                                                          KDS1; kinase domain related to Ste20; human; serine kinase;
                                                                                                                                                                                                                      Human KDS1 serine/threonine
                                                                                                                                                                                                                                                 10-MAY-1999
                                                                                                                                                                                                                                                                            AAW97676;
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           (CADU-) CADUS
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           PHARM CORP
                                      97US-0889518
                                                                  98WO-US14231
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71.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                      28-FEB-2000
                                                    AAY44244;
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THEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQE 121
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and drug screening.
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disorder; cirrhosis; cancer; hepatitis; AIDS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cell signaling proteins useful for, proliferative and inflammatory disorders
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26-AUG-1998;
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Yang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conservative
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98US-0098010.
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71.0%;
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Pred. No. 1.2e-1
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e-121;
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Query Match Best Local Similarity

70. . 98;

Score 1531.5; DB 2 Pred. No. 1.5e-121;

20;

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RESULT 12
AAY55936
cardiomyopathies, ischemic disorders, rurrummuss, end also mellitus, fibrotic and mesangial disorders. The proteins may also useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.
                                                                                                                           Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation, chronic inflammatory pelvic disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress related neurodegenerative disorders (e.g. amylotrophic lateral sclerosis, Parkinson's disease and Leigh sundrama
                                                                                                                                                                                                                                                                                                                        invention relates to nucleic acid molecule encoding a kinase polypeptide selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive; neuroprotective; cardiant; cerebroprotective; cytostatic; antidabetic; vulnery; STE20; protein kinase; STIK2; STIK3; STIK4; STIK5; STIK5; STIK7; ZC1; ZC2; ZC3; ZC4; KHS2; STIU1]; SULU3; GEK2; PAK4; PAK5; antagonist; antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma; inflammatory bowel disease; crohn's disease; osteoarthritis; psoriasis; rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure; oxidative stress-related neurodegenerative disorder; Parkinson's disease; oxidative stress-related neurodegenerative disorder; Parkinson's disease;
                                                                                                                                                                                                                                                          polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel kinase-related polypeptides used for the diagnosis and treatment of kinase-related diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY55936 standard; Protein;
                                                                                                       sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a novel STE20-related protein kinase. The
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ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
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04-FEB-2000;
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11-MAR-2000;
11-APR-2000;
11-APR-2000;
07-JUN-2000;
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07-JUN-2000;
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                                                                                                                                                                                                                                                                                                        17-JAN-2001;
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2000US-0198123.
2000US-0205515.
2000US-0205467.
2000US-0215135.
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17-NOV-2000;
autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 - NOV
                                                        The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include
                                                                                                                                        New isolated nucleic acid encod preventing, treating or amelior food additives or preservatives
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorder e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabe and pituitary dwarfism, cancers and disorders at the cellular level e.g.
                                                                                                                                                                23-MAR-2000;
11-JUL-2000;
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WPI; 2001-656860/75
                                                     Venter JC,
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Best Local
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                acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
                                                hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
                                                                                   Central nervous system; CNS;
                                                                                                                                     05-JUN-2002
                                                                                                                                                                                  AAU87435 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
    respiratory disorder; renal disorder;
                                                                                                           Novel central nervous system protein #345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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genes from D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABB57737-ABB72072)
                                                                                                                                                                                                                                            357 GVSAASSQSSSSNSIPAAAQN 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS 60
                                                                                                                                                                                                                                                                  SIS-ASSQSSSVNSLADASDN
                                                                                                                                                                                                                                                                                    VRELDNLNYRKNKKILMVDTCETESAVGDTDDQQDD---HAGGDSSKSNSITSEHSIHSV
                                                                                                                                                                                                                                                                                                       VRELDNLQYRKMKKILFQEAPNGPGAEAPEEEEEAEPYMHRAGTLT---SLESSHSVPSM
                                                                                                                                                                                                                                                                                                                                       ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA
                                                                                                                                                                                                                                                                                                                                                                                    {\tt SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPYFNMNAMSALYHIAQN}
                                                                                                                                                                                                                                                                                                                                                                                                SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGTTCIELAERKPPLFNMNAMSALYHIAQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                    KPLHEDETAAICLGVLSGLSYLHSLGRIHRDIKAGNILLTDNGVVKLADFGSAAIKCPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTGKQSQEKWQDILKEIRFLRQLNHPNTIEYKGCYLRESTAWLVMEYCVGSASDIIEVHK
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Drosophila and
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                                                                                                                                                                                 Protein;
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66.4%;
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Pred.
                                                                                   autoimmune disease; rheumatoid arthritis;
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No. 9
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    kidney failure; blood
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9.7e-102;
nes 72;
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18-AUG-2000

22-AUG-2000

22-AUG-2000

23-AUG-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
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17-MAR-2000;
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2000US-0225757 2000US-0225759 2000US-0225759 2000US-0225681 2000US-02268681 2000US-0227182 2000US-0227182 2000US-0227109 2000US-0229287 2000US-0229344 2000US-0229344 2000US-0229344 2000US-0229344 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-02314 2000US-023124 2000US-023124 2000US-023124 2000US-023124 2000US-023124 2000US-023141

2000US-0232401. 2000US-0233063. 2000US-0233064. 2000US-0233065.

2000US-0231968 2000US-0232397 2000US-0232398 2000US-0198123.
2000US-029467.
2000US-0216886.
2000US-0216847.
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2000US-02296.
2000US-025213.
2000US-025214.

2000US-0189874 2000US-0190076 2001WO-US01332

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KW myocardial infarction; wound healing; cell proliferation; skin aging;
KW food additive; food preservative; gene therapy.
XX
OS Homo sapiens.
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29-SEP-2000
02-OCT-2000
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03-OCT-2000
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2000US-0236368.
2000US-0236306.
2000US-0236370.
2000US-0237039.
2000US-0237039.
2000US-0237039.
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disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving nevvascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
                                                                                                                                                                                                                                                                                                    e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system
                                                                                                                                                                                                                                                                                                                                                                      e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaer angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, virus
                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders e.g. neoplasms of the breast or liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention describes an isolated nucleic acid molecule (I) encovel central nervous system protein. (I) and polypeptides (III) by (I), are used to treat a medical conditions and in diagnosis opathological condition. Disorders which are diagnosed or treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID No 953; 837pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing, tre food additives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                                                                                  g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders
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DB; ABK43765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid encoding a protein for diagnosing, or ameliorating medical conditions and used
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265;
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include

diabetes

as

δÃ B Ş B 80 멍 δÃ Query Best I Matches 121 151 61 91 YRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHGALQGLAYLHSHNMIHR Match Local Sines 210; 1 YKGCXLREHTXWLVMEYCLGSASDLLEVHKKPLQEVEIAAITHGALQGLAYLHSHTMIHR DVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVILAMDEGQYDGKVDVWS TSEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELDNLQYRKMKKILFQEAPNGPGAEAPE LGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNFVDSCLQKIPQDRP DIKAGNILLTEPGQYKLADFGSASMASPANSFYGTPYWMAPEVILAMDEGQYDGKYDYWS LGITCIELAERKPPLFNMNAMSALYHIAQNESPTLQSNEWSDYFRNFVDSCLQKIPQDRP Similarity Conservative 51.8%; 87.5%; 11; Score 1119; DB 22; Pred. No. 3.9e-87; Mismatches 19; Indels 0; Gaps 60 150 180 120

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Search completed: November Job time: 30.376 secs 22, 12:23:42

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Maximum Match 100%
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                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                            SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe!(
9: sp_phage:*
10: sp_plant:*
11: sp_vinus:*
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
15: sp_varchea;
16: sp_bacteri
17: sp_archeap
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Gapop 10.0 , Gapext 0.5
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1678
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sp_mammal:*
                                   SUMMARIES
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Result No.	Score 1678 1674	Query Match 100.0	Query Match Length DB 100.0 1235 1	DB 11	ID Q9JLS3 Q94957
		99.8 91.1	1235	1 4	Q9UL54
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7		83.1	868	13	Q919E0
œ		83.0	898	4	Q9UHG7
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10		82.8	898	4	Q9NZM9
11		82.4	898	4	Q9H2K8
12	1239.5	73.9	1039	ഗ	Q9VWG8
Ξ	703	41.9	398	4	Q9H7S5
14	640	38.1	842	10	Q9FNU3
15	631.5	37.6	836	10	024527
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Q9nb31 caenorhabdi		Q9ven3 drosophila	homo	homo	homo	homo	. Q9uke3 homo sapien	homo	Q9ukel homo sapien			Q95zn6 caenorhabdi	ratt		mus	OMO	Q9ji10 mus musculu	Q60877 mus musculu	062571 suberites d		Q9v8w4 drosophila	Q9ji11 mus musculu		dict			triticu	Q9arl7 hordeum vul

### ALIGNMENTS

PRELIMINARY; PRT; 1235 AA.  (TrembLrel. 15, Created) (TrembLrel. 20, Last sequence update) (TrembLrel. 20, Last annotation update) conine protein kinase TAO2.  regicus (Rat).  Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; sutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus10116;  ROM N.A.  128563; PubMed=10497253; Itchison M., Cobb M.H.; of the protein kinase TAO2 and identification of its of the protein kinase/extracellular signal-regulated kinase ling domain."; nem. 274:28803-28807(1999).  ROM N.A.  ROM N.A.  ROM N.A.  ROM N.A.  ROM N.A.  ROM N.A.  ROM SELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  13TY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  11: 1138  ROM SET_thr_pkinase.  IPR001290; Ser_thr_pkinase.  IPR001245; Tyr_pkinase.  IPR001245; Tyr_pkinase.  IPR001245; Tyr_pkinase.  IPR001345; GRAM_POS_ANCHORING; UNKNOWN_1.  100343; GRAM_POS_ANCHORING; UNKNOWN_1.	HSSP; P2 InterPro InterPro InterPro InterPro InterPro InterPro InterPro PRIMIS; PRODOM; PROSITE; PROSITE; PROSITE;			GN TAUZ.  OS Rattus norvegicus ( CEUkaryota; Metazoa; CC Mammalia; Eutheria; CX NCBI_TaxID-10116; EN [1]	DT 01-0CT-2000 DT 01-0CT-2000 DT 01-0CT-2000 DT 01-MAR-2002 DE Serine/thre	JLS
î î	; Euk_pkinase.; Gram_pos_anchor.; Ig_MHC.; Ser_thr_pkinase.; Tyr_pkinase.; Tyr_pkinase. ase; 1. RKINASE. uk_pkinase; 1. uk_pkinase; 1. KC; 1. RAM_POS_ANCHORING; G_MHC; UNKNOWN_1.	M., Cobb M.; ) to the EMBL/GenBank/DDBJ databases. ) ONGS TO THE SER/THR FAMILY OF PROTEIN 139480.2;	PubMed=10497253;  M., Cobb M.H.;  protein kinase TAO2 and identification of its protein kinase/extracellular signal-regulated nain."; 1:28803-28807(1999).	Rat). Chordata; Rodentia;	(TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 20, onine protein kin	PRT; 1235

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    Submitted (MAY-2000) to the EMBL/GenBank/
-!- SIMILARITY: BELONGS TO THE SER/THR FA
EMBL; AB020688; BAA74904.1; -.
EMBL; AF263313; AAG38503.1; -.
EMBL; AF263313; AAG38503.1; -.
EMBL; AF263713; BAG38503.1; -.
EMBL; AF263313; AAG38503.1; -.
EMBL; AAG38503.1; -.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
KIAA0881 protein (STE20-like kinase).
                                                                                                                                                                                               Yustein J.T., Robinson D., Templeton D.J., "Characterization of a Subfamily of Human S Selectively Activate p38 Through MKK3 and a dependent Mechanism.";
                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99156230; PubMed=10048485;
Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
The complete sequences of 100 new cDNA clones from brain which co
for large proteins in vitro.";
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PROSITE; PS00101; PROTEIN_KINĀSE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINĀSE_ST; 1
ATP-binding; Kināse; Serine/Khreonine-protein kināse; Transferase.
SEQUENCE 1235 AA; 138750 MW; 426960D0812518AD CRC64;
  Pfam;
                                                                                                                                                                                                                                                                                                                                         DNA
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Mammalia; Eutheria;
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no sapiens (Human).
Netazoa; Chordata; C;
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THE SER/THR FAMILY
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Pred. No. 3.4
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Q9UL54;
Q9UL54;
01-MAY-2000 (TrEMBLrel. 13, C)
01-MAY-2000 (TrEMBLrel. 13, La
01-MAR-2002 (TrEMBLrel. 20, La
Prostate derived STE20-like k:
                                                                  Pfam; PF00069; pkinase; I.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S.TKC; 1.
                                                                                                                                                                                                                                          organisation.";
J. Biol. Chem. 275:4311-4322(2000)
-:- SIMILARITY: BELONGS TO THE SER
EMBL; AF061943; AAD45616.1; -.
HSSP; P24941; 1B38.
    PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20127920; PubMed=10660600;
Moore T.M., Garg R., Johnson C., C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                             InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                              "PSK, a novel STE20-like kinase derived from activates the JNK MAPK pathway and regulates
                                                                                                                                                                                                                                                                                                                                                                                                                 Morris J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=BREAST CARCINOMA;
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SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1

PROSITE; PS50011; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-p
                                                                                                                                                                InterPro; IPR001245; Tyr_pkinase
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Hutchison M., Berman K.S., Cobb M.H.;
I "Isolation of TAO1, a protein kinase that activates MEN
I activated protein kinase cascades.";
J. Biol. Chem. 273:28625-28632(1998).
--- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEI
EMBL; AF084205; AAC71014.1; --
EMBL; AF084205; 
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01-NOV-1998 (TIEMBLIE) 08, Last sequence update)
01-MAR-2002 (TIEMBLIE) 20, Last annotation update)
Serine/threonine protein kinase TAO1.
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SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Kinase; Serine/threonine-protein kinase; SEQUENCE 1001 AA; 115952 MW; 85511B62DBD62FCC CRC
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SEQUENCE 1005 AA; 116540 MW; A83BD4!
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Mammalia; Eutheria; F
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PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
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MEDLINE=20181126; PubMed=10718198;

Magase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human genes.XVI.

The complete sequences of 150 new cDNA clones from brain which code

for large proteins in vitro.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Maracterization of a Subfamily of Human STE20-Selectively Activate p38 Through MKK3 and are Reg. T dependent Mechanism.",

L Submitted (MAY-2000) to the EMBL/GenBank/DDBJ da+1 HSSP; P24941; 1B38.

InterPro; IPBAAAA.
                                                                                                                                                                                                                                                                                                      Query
Best I
                                                                                                                                                                                                                                                                               Matches
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SMART; SM00220; S_TKC; 1.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATD;

PROSITE; PS0011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                     Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR00169; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STE20-like kinase (Fragment).
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                     KPLQEVETAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN
                                                                                  KPLQEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN
                                                                                                                                                                              MPSTNRAGSLKDPEIAELFFKEDPEKLFTDLREIGHGSFGAVYFARDVRTNEVVAIKKMS
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1001 AA;
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88.4%;
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                                                                                                                                                                                                                                                                        Score 1519; DB 4;
Pred. No. 3.5e-126;
2; Mismatches 15;
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0919E0;
019CP-2000 (TremBLrel. 1
01-OCT-2000 (TremBLrel. 1
01-MAR-2002 (TremBLrel. 2
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SEQUENCE
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SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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KPC (Fragment).

Gallus gallus (Chicken).

Fusianidae; Phasianidae; Phasianidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=20162342; PubMed=10698516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002290; Ser_thr_pking
InterPro; IPR000130; zn_MTpeptdse
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306 NLQYRKMKKILFQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase;
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es 258; Conserv
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Pred. No. 3.9e
30; Mismatches
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OPUNG7
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Best Local S
Matches 257
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Interpro; IPR002299; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Interpro; IPR001013; Zn_MTpeptdse.
Pfam; PF00069; pkinase; 1.
PRINTS; PR001109; TYRKINASE.
PRODom; PD000001; Euk_pkinase; 1.
PRODom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00111; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00113; PROTEIN_KINASE_ST; 1.
PROSITE; PS001142; ZINC_PROTEASE; UNKNOWN 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
     Q9HC79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES EMBL; AF179867; AAF14559.1; -. HSSP; P24941; 1B38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human JIK, a novel member of the James and is negatively regulated by epidermal growth J. Biol. Chem. 274:33287-33295(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=20026851; PubMed=10559204;

Tassi E., Biesova Z., Di Fiore P.P., Gutkind J.

"Human JIK, a novel member of the STE20 kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STE20-like kinase
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01-MAR-2002
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01-MAY-2000
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Mammalia; Eutheria; Primates;
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SEQUENCE 898
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THEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQE 121
                                                                                                                                                   NLQYRKMKKILFQE
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                                                                                                                            NLQYRKMKKILFQE
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                                                                                                                                                                                                                                                                                                                  PYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSPTL
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     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinase; Serine/threonine-protein kinase; 98 AA; 105657 MW; 61F04628713E6025 CRC6
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Pred. No. 5.9e-115;
1; Mismatches 26;
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     PRT;
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e family that i
growth factor."
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PRODOM; PD000001; Euk_Pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM002219; TYRC; 1.
SMART; SM00219; TYRC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS050011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
ATP-binding; Kinase; Transferase.
ATP-binding; Kinase; Transferase.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Serine kinase (STE20-like kinase).
Q9NZM9;
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000130; Zn_Wrpeptdse.
Pfam; PF00069; pkinase; 1.
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MEDLINE-20384190; PubMed=10924369;

Zhang W., Chen T., Wan T., He L., Li N., Yuan Z.,

"Cloning of DPK, a novel dendritic cell-derived pp
activating the ERK1/ERK2 and JNK/SAPK pathways.";

Biochem. Biophys. Res. Commun. 274:872-879(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2001) to the EMBL; AF135158; AAG09131.1; EMBL; BC002756; AAH02756.1; HSSP; P24941; 1B38.
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Local
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                                                                 NLQYRKMKKILFQE
                                                                             NLQYRKMKKILFQE
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          PRELIMINARY;
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Pred. No. 5.9e
81; Mismatches
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          PRT;
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          898
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5.9e-115;
les 26;
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Best Local Similarity
Matches 256; Conserv
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PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_PKinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500142; ZINC_PROTEASE; UNKNOWN.1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.
            Q9H2K8 PRELIMINARY; FQ9H2K8;
Q9H2K8;
Q1-MAR-2001 (TrEMBLrel. 16, Cre
Q1-MAR-2001 (TrEMBLrel. 21, Las
Q1-UN-2002 (TrEMBLrel. 21, Las
STE20-11ke kinase (Fragment).
Homo sapiens (Human).
  Eukaryota;
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HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carter T.G., Benton B., Fruhling D., Monks C.R.F., Windmiller D., Kupfer A., Manfredi J., Johnson G.L., Pleiman C.M.;
"KDS and TAO1, two related proteins with kinase domain homology to STE20, differentially relocate in mitogen stimulated T lymphocytes.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Serine/threonine kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002299; Ser_thr_pkin
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000130; Zn_MTpeptdse
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                                                                                                                                              NLQYRKMKKILFQE
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                                                                                                                                                                                                       QSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELD
                                                                                                                                                                                                                                       PYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSPTL
                                                                                                                                                                                                                                                     PYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPAL
                                                                                                                                                                                                                                                                                       VEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGT
                                                                                                                                                                                                                                                                                                                                      THEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQE
                                                                                                                                                                                                                                                                                                                                                                                    AF181985; AAF25817.1; -. P24941; 1B38.
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 Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kinase; Serine/threonine-protein kinase; Transferase. 98 AA; 105432 MW; 9738BD5DCFA12AC9 CRC64;
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Primates;
  Chordata;
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Tyr_pkinase.
Zn_MTpeptdse.
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81.5%;
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Pred. No. 1.1e
32; Mismatches
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Last sequence update)
Last annotation updat
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                                    sequence update) annotation updat
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Vertebrata;
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                                    update)
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Euteleostomi;
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Best Local S
Matches 255
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                                                           Q9VWG8 PRELI
Q9VWG8;
Q1-MAY-2000 (TrEM
01-MAY-2000 (TrEM
01-MAR-2002 (TrEM
CG14217 protein.
CG14217;
              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PTODOM; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYFKC; 1.
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PROSITE;
PROSITE;
PROSITE;
Kinase.
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SEQUENCE FROM N.A
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                             QSNEWTDSFRRFVDYCLQKIPQERPTSAELLRHDFVRRDRPLRVLIDLIQRTKDAVRELD
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00107; PROTEIN_KINASE_ATP;
PS50011; PROTEIN_KINASE_DOM;
PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00142; ZINC_PROTEASE; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FROM N.A
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                                                                            (TrEMBLrel.) (TrEMBLrel.)
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868
                                                                                                                 PRELIMINARY;
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105501 MW;
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81.2%;
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13,
20,
                                                                           Last sequence update)
Last annotation update)
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l; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                           Score 1383;
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ly of Human
jh мкк3 and
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                                 Muscomorpha;
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RA Abrill J.F., Agbayani A. An H.-J., Andrews-Pfannkoch C.K., MALSIOS G.L.G., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Botshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Ra Borkova D., Datchan R., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA Cherry J.M., Cawley S., Dahlke C., Duyan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Godson K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P., RA Godson K., Cong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Jalali M., Kalush F., Karpen G.H., KE Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lin X., Jalali M., Kalush F., Karpen G.H., KE Z., Kennison J.A., Ketchum K.A., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA McIntov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., McIntov B.R., Nilshina N.V., Nobarry C., Morris J., Moshrefi A., McIntov B.R., Nilshina N.V., Stapleton M., Skupski M.P., Smith T., RA Shie B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., RA Shie B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., Ra Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X., Yao Q.A., Yah G., Pens J., Pollard J., Pens S., Yao Q.A., Kan Shie B., Kan M., Weissenbach J., Ra Wang Z.-Y., Wassarman D.A., Weissenbach J., Ra Wang Z.-Y., Kan Shie B., Ra Napis South S., Shie M., Shie B., Shie B., Shie B., Shie B., Shie B., Shie B., Shi
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Best Local
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InterPro; IPR0007719; Euk_pkinase.
InterPro; IPR000299; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Transferase
       180
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SFYGTPYWMAPEVILAMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS 60
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73.7%;
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Qy

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Qy Db QΥ

Вb

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RESULT 13
Q9H7S5
ID Q9H7S
AC Q9H7S
DT Q1-M2
DT Q1-M2
DT Q1-M2
DT Q1-M2
DE CDNA
DE Serii
OS Homo
OC Euka
OC Mamm
OX NCBJ
RN [1]
RP SEQJ
RC TIS
RA Nis
RA Nis
RA Nis
RA Tan
RA Ari
RA Wal
RT "N'
RL Su'
DR EM
DR In
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DR PJ
DR SI
DR PJ
RESULT 14
QOPNUS
ID QOPNUS
AC QOPNUS
DT 01-MA
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DT 01-MA
DT 01-MA
COS OTYZA
OC EUKART
OC EUKART
OC ENTHA
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Best Local :
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01-MAR-2001
01-MAR-2001
01-MAR-2002
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Q9H7S5;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 20, Last and
O1-MAR-2002 (TrEMBLrel. 20, Last and
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Oryza sativa (kıc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AR024376; BAB14901.1; "InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000719; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel 16, Last sequence update)
01-MAR-2002 (TrEMBLrel 20, Last annotation update
CDNA FLJ14314 fis, clone PLACE3000350, weakly simil
serine/threonine-protein kinase SULU (EC 2.7.1.-).
                                   Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S.TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                            3615.3
                                                                                                                                                                                                  Q9FNU3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Ti
SEQUENCE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=PLACENTA;
Isogai T., Ota T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                             297
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                                                                                                                                                                                                                                                                                                                                                                                                    237
                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APANSFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYH 236
                                                                                                                                                                                                                                                                                                              TKDAVRELDNLQYRKMKKILFQEA 320
                                                                                                                                                                                                                                                                                                                                                                                 IAQNESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRELDNLNYRKMKKIL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRELDNLQYRKMKKIL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA
                                                                                                                                                                                                                                                                                         TKDAVRELDNLQYRKMKKLLFQEA 146
                                                                                                                                                                                                                                                                                                                                                              IAQNESPTLQSNEWTDYFRNFVDSCLQKIPQDRPTSEELLKHIFVLRERPETVLIDLIQR
                                                                                                                                                                                                                                                                                                                                                                                                                                     SPANSFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132;
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                                                                                                                                             (TrEMBLrel.
                                                                   (Rice).
iridiplantae;
                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                   PRELIMINARY;
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98 AA; 46177 MW;
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91.7%;
                                                                                                                           16,
16,
20,
                                                                      Streptophyta;
                                                                                                                           Created)
Last sequence up
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Pred. No. 3.7e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                       Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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RESULT 15
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ID 02452
AC 02452
DT 01-JA
DT 01-MA
DT 01-MA
DT Serin
GN SIK1
OC Eukar
OC Sperin
OC Sperin
OC Sperin
OC SPERI
RN [1]
RP SEQUE
RC STRAI
RN [2]
RP SEQUE
RA Winge
RA Winge
RA SIZAI
RN [2]
RP SEQUE
RC STRAI
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Best Local Similarity
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Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR002290; Ser_thr_pkinase.
Interpro; IPR001245; Tyr_pkinase.
Pfam; PP00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00210; TyrKC; 1.
SMART; SM00211; TyrKC; 1.
PROSITE; PS00117; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00117; PROTEIN_KINASE_DOM; 1.
ATP-binding; Transferase.
SEQUENCE 842 AA; 91646 MW; EBE222157E4
                                                                                                                                                                                                                                                                                                                                                                                          024527

024527;

01-JAN-1998 (TremBLrel. 0:

01-JAN-1998 (TremBLrel. 0:

01-MAR-2002 (TremBLrel. 2:
                                                                               Winge P.,
Submitted
                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eveurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE; TRANSPOSON-GAIGAN;

MEDLINE-21140318; PubMed=11244114;

Dubcovsky J., Ramakrishna W., SanMiguel P.J., Busso C.S., Yan L.,

Shiloff B.A., Bennetzen J.L.;

"Comparative sequence analysis of colinear barley and rice bacterial artificial chromosomes.";

Plant Physiol. 125:1342-1353(2001).

EMBL; AV013245; AA645491.1; -.

HSSP; Q63450; 1A66.
SEQUENCE FROM N.A. STRAIN=CV. COLUMBI
                                                                                                                                   STRAIN=CV.
                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                 Serine/threonine kinase.
SIK1 OR F23010.20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLKHRFVLRERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEPGLYKLGDFGSAS----IMAPANSFYGTPYWMAPEVILAMDEGQYDGKYDVWSLGITC
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                                                                            Brembu T.,
1 (APR-1997)
                                                                                                                        COLUMBIA;
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                                                                            Bones A.M.
to the EMB
                                                                                                                                   TISSUE-HYPOCOTYL;
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20,
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Last annotation update)
                                                                               EMBL/GenBank/DDBJ databases
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Pred. No. 4.3e-48;
6; Mismatches 91;
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Best Local S
Matches 127
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EMBL: U96313, AAB68766.; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; ATP-binding; Kinase; Transferase.
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SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
pfam; PF00069; pkinase; 1.
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HSSP; Q00534; 1B18
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                                                                          RNFVDSCLQKIPQDRPTSEVLLKHRFVLR
                                                                                                                                AMDEGQYDGKVDVWSLGITCIELAERKPPLFNNNAMSALYHIAQNESPALQSGH-WSEYF
                                                                                                                                                                         AYLHSIYKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVI-
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                                                          HDFVAKCLTKEPRLRPTAAEMLKHKFVER
                                                                                                                                                                                                                                  QQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVADLMNVTEEALEEYQIAYICREALKGL
                                                                                                                  -- QENRYDGKVDVWALGVSAIEMAEGLPPRSSVHPMRVLFMISIEPAPMLEDKEKWSLVF
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             22,
             2002,
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                                                                                                                                                                                                                                                                                                                                                                  Score 631.5; DB 10; Length Pred. No. 2.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                             805F18FDFA430762 CRC64;
             12:26:13
                                                                                                                                                                                                                                                                                                                                                    Mismatches
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77;
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Title:
Perfect score:
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Maximum DB
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match Length
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ALIGNMENTS	NEK3_HUMAN	M3K1_MOUSE	M3K1_HUMAN	M3K1_RAT	M3K2_MOUSE	M3K2_HUMAN	BCK1_YEAST	NINC_DROME	M3K3_MOUSE	M3K3_HUMAN	CC15_YEAST	WIS4_SCHPO
	P51956 homo sapien	P53349 mus musculu	Q13233 homo sapien	Q62925 rattus norv	Q61083 mus musculu		Q01389 saccharomyc					014299 schizosacch

## RESULT 1 SULU\_CABEL SULU\_CABEL ID SULU\_C AC P46549 DT 01-NOV DT 16-OCT DE SCAENOR OC ENKARY OC Rhabdi OX CAENOR RA DU Z. RL SUBMIT RN [1] RP SEQUEN RC STRAIN RA SUBMIT CC ---RL SUBMIT CC This SC CC the Eu CC The Eu CC Use th CC Use th CC Use th CC DETME CC THIS CC THIS CC THIS CC TOTSE CC SULU\_CAEEL STANDARD; PRT; 982 AA. 946549; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Serine/threonine-protein kinase SULU (EC 2.7.1.-). KIN-18 OR SULU OR T17E9.1. EMBL; U11280; AAA19437.1; -. EMBL; U31275; AAA75370.1; -. WormPep; T17E9.1; CE01405. InterPro; IPR000719; Euk\_pkinase. InterPro; IPR002290; Ser\_thr\_pkinase. Pfam; PF00069; pkinase; 1. STRAIN-Bristol N2; Cope M.J.T.V., Kendrick-Jones A.; Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. or send an email to license@isb-sib.ch). NCBI\_TaxID=6239; Pfam; PF00069; pkinase; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ STRAIN-Bristol N2; SEQUENCE FROM N.A. SEQUENCE FROM N.A. databases

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6 RAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQ

Query Match
Best Local Similarity
Matches 184; Conserv

Conservative

57;

Score 1008; DB 1; Pred. No. 3.4e-68; 7; Mismatches 71;

Length 982; Indels

6,

Gaps

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60.1%; 57.9%;

PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

PROSITE; PS00108; PROTEIN\_KINASE\_T; PALSE NEG.

Transferase; Serine/threonine-protein kinase; ATP-binding.

DOMAIN

30
289
PROTEIN KINASE
NP\_BIND
36
44
ATP (BY SIMILARITY).

BINDING
59
ACT\_SITE
153
153
BY SIMILARITY.

SEQUENCE
982 AA; 112870 MW; 745CE1E2F890977D CRC64;

ProDom; PD000001; Euk\_pkinase; 1.
SMART; SM00220; S\_TKC; 1.

PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

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    the
            between
             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                "Identification of a human brain-specific isoform of mammalian STB20-like kinase 3 that is regulated by cAMP-dependent protei
                                                                                                                                                                                                                                                                                                         Zhou
                                                                                                                                                                                                                                                                                                                    MEDLINE=20112812;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM B), AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and characterization of a human cofactor requirements.";
                                                                                                                                                                                                                                                                                                                                                                                                              Schinkmann
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98019249; PubMed-9353338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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ST24_HUMAN
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European
                                                 BY PKA.
SIMILARITY: BELONGS TO
STE20 SUBFAMILY.
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                                                                                                                                            SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein COFACTOR: ISOFORM A REQUIRES MANGANESE FOR ITS ACTIVITY.
                                                                                                                                 TISSUE SPECIFICITY: ISOFORM A IS UBIQUITOUS. ISOFORM
                                                                                                                      EXPRESSED IN BRAIN WITH
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m. 272:28695-28703(1997).
  Swiss Institute
Bioinformatics 1
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PROTEIN KINASE THAT ACT
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                                                                                                                     HIGH EXPRESSION
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile stress-response kinase 1) (Ste20/oxidant stress response k
[SOK-1] (Ste20-1ike kinase).

kinase-1)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Sciurognathi;

Murinae;

Mus musculus (Mouse) STK25 OR SOK1

NCBI\_TaxID=10090;

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ST25_
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                                                  RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001245; Tyr_pkinase.

Pfam; PF00069; pkinase; 1.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; FAI

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation;
DOMAIN 36
NP_BIND 42
BINDING 65
ACT_SITE 156
MOD_RES 18
VARSPLIC 1
                         _MOUSE
ST25_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
SEQUENCE
Q9Z2W1;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF024636; AAB82560.1;
EMBL; AF083420; AAD42039.1;
HSSP; P24941; 1CKP.
Genew; HGNC:11403; STK24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002290; Ser_thr_pkir
InterPro; IPR001245; Tyr_pkinase
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase;
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                                                                                                                                                                                     145
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                                                                                                                                                                                                                                                                                               KDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFL
                                                                                    EFVEACLNKEPSFRPTAKELLKHKFILRNAKKTSYLTELIDRYK
                                                                                                          NFVDSCLQKIPQDRPTSEVLLKHREVLRERPPT-VIMDLIQRTK 298
                                                                                                                                                  AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFR : | | | | | | | | | | | : | : : : :
                                                                                                                                                                                                     AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL
                                                                                                                                                                                     DYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI-
                                                                                                                                                                                                                                    SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL
                                                                                                                                                                                                                                                  QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
                                                                                                                                                                                                                                                                                  KADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAIKIIDL--EEAEDEIEDIQQEITVL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             604984;
                                                                                                                                                                                                                                                                                                                                     130;
                                                                                                                                      KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                18
414
443
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                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine/threonine-protein kinase; ion; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                    ΑA;
                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN_KINASE_ST; FALSE_NEG
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45.8%;
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                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                   Score 594; DB Pred. No. 1.6e
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A -> V
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MDSRAQLWGLALNKRRATLPHPGGST
GMQ (IN ISOFORM A).
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ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE
                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                 LOSS OF PHOSPHORYLATION V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                DB 1;
..6e-37;
                         B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                                                                                         Length 443
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RESULT 4
ST25_HUMAN
ID ST25_H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation.
DOMAIN 20
NP_BIND 26
BINDING 49
ACT_SITE 140
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
   ST25_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genetic mapping of human and mouse PAK genes.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE;
ProDom; PD000001; Euk pkinase; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ATP + a p
ENZYME REGULATION: ACTIVATED
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                                                                                                                                                                                                                  DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF : | | : | : | | : | : | : | : |
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                                                                                                                                                                             VEACLNKDPRFRPTAKELLKHKFITRYTKKTSFLTELIDRYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine/threonine-protein kinase; ATP-binding;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN_KINASE_DOM;
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O THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 580; DB 1;
Pred. No. 1.8e-36;
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ATP (BY SIMILARITY).
BY SIMILARITY.
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   PRT;
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There are no restrictions
ong as its content is in
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Query Match
Best Local Sin
Matches 128;
                                                                        Phosphorylation.
DOMAIN 20
NP_BIND 26
BINDING 49
ACT_SITE 140
CONFLICT 347
                                                                                                                                                                                                                                                                                                                       EMBL; X99325;
EMBL; D63780;
HSSP; P12931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97304522; PubMed-9160885;
MEDLINE-97304522; PubMed-9160885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant stress-response kinase 1) (Ste20/oxidant stress response kinase-1)
(SOK-1) (Ste20-like kinase).
                                                                                                                                                                                                                                                                                               MIM;
                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.
-!- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
-!- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY
AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97042345; PubMed=8887545; Pombo C.M., Bonventre J.V., Molnar A., Kyriakis "Activation of a human Ste20-like kinase by oxio
                                                                                                                                                                             PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                    ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                             InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE KINASE ACTIVITY.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- TISSUE SPECIFICITY: UBIQUITOUSLY E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and SPS1, but is not involved in the known MAPK pathways."; Oncogene 14:2047-2057(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          novel stress response pathway.";
EMBO J. 15:4537-4546(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                     Pfam; PF00069;
                                                                                                                                                                                                                                                                                                           Genew; HGNC:11404;
                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STK25 OR SOK1 OR YSK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             000506; Q15522;
                                                                                                                                                                 Fransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND HEART AND LUNG.
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                                                                                                                                                                                                                                                                                               602255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a novel mammalian protein kinase structurally
                  Similarity
                                                                                                                                                                                                         PS00108; PROTEIN_KINASE_ST; FALSE_NEG
                                                             426
    Conservative
                                                                                                                                                              Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                         1FMK.
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                                                                                                                                                                                                                                                                                                                                        BAA20420.1;
                                                             ÀΑ;
                                                                                                                                                                                                                                                    pkinase;
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                                                                         270
34
49
140
348
                                                             48111 MW;
                  34.38;
    48;
                                                                                    PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                Score 576;
Pred. No. 3.
                                                                           ΕP
                                                            183CE5700FCEA716 CRC64;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mizuno K.,
                                                                           DA (IN REF. 1)
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                DB 1;
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oxidant
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                              Length 426;
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Oliological force
DE Serine
DE SERINE
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GN STK4 O
OS Homo S
OC Eukary
OC MARMAI
DE (Serin
RA FIT)
RN [1]
RR Creasy
RR MEDLIN
RA Creasy
RR SEQUEN
RX MEDLIN
RA Taylor
RN [2]
RP SEQUEN
RX MEDLIN
RA Taylor
RN [3]
CC -!- SI
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CC -!- SI
C
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Q13043; Q15802; Q9NTZ4;
Q13043; Q15802; Q9NTZ4;
16-OCT-2001 (Rel. 40, Cast sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine protein kinase 4 (EC 2.7.1.37) (STE20
MST1) (MST-1) (Mammalian STE20-like protein kinase 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96413604;
   EMBL; U18297; AAA83254.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taylor L.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and characterization of a human to Ste20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Creasy C.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95394929; PubMed=7665586; Creasy C.L., Chernoff J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Cytoplasmic (By similarity). TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way in the state of the st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                           SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sci. U.S.A. 93:10099-10104(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stress-responsive protein kinases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H.C., Erikson R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=8816758;
                                                                                                                                                                                                                                                                                                                                                                                                                           SERINE AND THREONINE RESIDUES SER/THR FAMILY OF PROTEIN KIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in = ADP + a phosphoprotein NON-CATALYTIC REGION INHIB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein kinase with homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .37) (STE20-like kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krs-1 and
                                                                                                                                                                                                                                                                                                                                                                                                                               KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHIBITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krs-
                                                                                                                                                       in no way
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STK3_HUMAN
ID STK3_H
AC Q13188
DT 16-OCT
DT 16-OCT
DT Serine
DE Serine
QE (Serin
GN STK3 0
OS HOMO S
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RX MEDLIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                              HUMAN STANDARD; PRT; 491 Am. STX3_HUMAN STANDARD; PRT; 491 Am. Q13188; Q15801; Q15445; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Serine/threonine protein kinase 3 (EC 2.7.1.37) MST2) (MST-2) (Mammalian STE20-like protein kina MST2) (MST-2) (MST-2) (Mammalian STE20-like protein kina MST2) (MST-2) (MST-2
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PROSITE;
PROSITE;
                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
    MEDLINE=96144292; Pub
Creasy C.L., Chernoff
                                                                                                                                                             STK3 OR MST2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genew; HGNC:11408; STK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U60207; AAB17262.1;
EMBL; AL109839; CAB89421.
HSSP; P24941; 1HCL.
                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNTVIGTPFWMAPEVI---QEIGYNCVADIWSLGITAIEMAEGKPPYADIHPMRAIFMIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604965;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTEDEIATILQSTLKGLEYLHFMRKIHRDIKAGNILLNTEGHAKLADFGVAGQLTDTMAK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRNPPRRQLKKLDEDSLTKQPEEVFDVLEKLGEGSYGSVYKAIHKETGQIVAIKQVPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ESDLQEIIKEISIMQQCDSPHVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00108; PROTEIN_KINASE_ST; FALSE_NEG PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002290; Ser_thr_pkin
IPR001245; Tyr_pkinase.
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373
222
312
487 I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine-protein kinase; ATP-binding.
30 281 PROTEIN KINASE.
36 44 ATP (BY SIMILARITY).
59 59 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pkinase;
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                       PubMed=8566796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
59
149
378
222
312
                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312
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ATP (BY SIMILARITY).
BY SIMILARITY.
POLY-GLU.
P -> R (IN REF. 1).
V -> M (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 574; DB 1;
Pred. No. 5.8e-36;
                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150758EBC5F77D5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                    Hominidae;
                                                                                                                                                                                                                                .37) (STE20-like kinase kinase 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116;
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                                                                                                                                          Euteleostomi;
                                                                                                                    Homo
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QΥ 멼 Ω В Ω В δÃ

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Query Match
Best Local S
Matches 120
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EMBL; Z25422; C
HSSP; P24941;
"CNC:11
                                                                                                                                                                                                                                                                       CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restruct by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schultz S.J., Nigg E.A.;
Schultz S.J., Nigg E.A.;
"Identification of 21 novel human protein kinases, including 3 members of a family related to the cell cycle regulator nimA of Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-96413604;
Taylor L.K., Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and characterization Ste20-like kinases.";
                                                                                                                                                                                                                                               SEQUENCE
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene 167:303-306(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
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Newly identified
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                                                                 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT KIDNEY, SKELETAL AND PLACENTA TISSUES AND AT VERY LOW LEVELS IN ADULT KIDNEY, STALLARITY: BELONGS TO THE STALLARITY: BELONGS TO T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES STE20 SUBFAMILY.
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                                                          PEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQKL 83
   PEEVFDVLEKLGEGSYGSVFKAIHKESGQVVAIKQVPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U26424;
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                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pkinase;
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stress-responsive p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci. U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'threonine-protein kinase; ATP-binding.
778 PROTEIN KINASE.
41 ATP (BY SIMILARITY).
56 ATP (BY SIMILARITY).
                                                                                                                                                     33.8%;
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N THE RESPONSE TO
                                                                                                                                                                                                                                               MW:
                                                                                                                                                                                                                                     POLY-GLU.
POLY-GLU.
WIV -> YLY (IN REF. 3).
D -> Y (IN REF. 3).
D -> G (IN REF. 3).
D -> E (IN REF. 2).
D -> E (IN REF. 2).
GEC -> ESV (IN REF. 3).
GEC -> ESV (IN REF. 2).
                                                                                                                                                     Pred.
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                                                                                                                     ced. No. 2e-35;
Mismatches 1
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ESDLQEIIKEISIMQQC
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EMBL outstation

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ILRELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED GTPASES TO THE JNK MAP KINASE PATHMAY.

ILRELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED GTPASES TO THE JNK MAP KINASE PATHMAY.

I. SUBUNIT: INTERACTS TICHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RAC1 (BY SIMILARITY).

I. TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BRAIN, WI HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH MOTOR FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.

I. DEVELOPMENTAL STACE: FOUND IN THE EMBRYONIC CNS WITH LITTLE
               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.
Kinase 1) (PAK-1) (P68-PAK) (Alpha-PAK) (Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAT
                                                                     -!- PTM: AUTOPHOSPHORYLATED -!- SIMILARITY: BELONGS TO T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94150588; PubMed=8107774; Manser E., Leung T., Salihuddin H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P35465; Q62
                                                                                                                                                                                                                                       J. Biol.
                                                                                                                                                                                                                                                     kinase
                                                                                                                                                                                                                                                                                                        MEDLINE=96027610;
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                                                                                                                                                                                                                                                                                           Manser E.,
                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 367:40-46(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                "Molecular cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      brain serine/threonine
                                         STE20 SUBFAMILY SIMILARITY: CON
                                                                                                  EXPRESSION ELSEWHERE
    SWISS-PROT entry is copyright.
een the Swiss Institute of Bio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKKCLVKNPEQRATATQLLQHPFIKNAKPVSILRDLITEAMEIKAKRHDEQQRELEE
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                                                                                                                                                                                                                                                                                                                                                                           S.-I.,
                                                                                                                                                                                                                                                  (PAK) family.
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                                                                                                                                                                                                                                     Chem.
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                                                                                                                                                                                                                                                                                           Chong
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                                          CONTAINS 1
                                                                                                                                                                                                                                                                                          C.,
                                                                                                                                                                                                                                                                                          PubMed=7559638;
C., Zhao Z.-S.,
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Rodentia;
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protein kinase activated
                                            CRIB
                                                                       THE
                                                                                  WHEN ACTIVATED
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                                                                       SER/THR
gnt. It is produced Bioinformatics and
                                            DOMAIN
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                                                                                                                                                                                                                                                                                          Leung
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                                                                       FAMILY
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                                                                                                                                                                                                                                                                                          Michael G.,
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kinase MUK2).
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                                                                       KINASES
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            collaboration
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RESULT MA
PAKI_H
PAKI_H
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DT 01-NOV
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DE Serine
E kinase
GN PAK1.
OS Homo S
OC Eukary
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RP SEQUEN
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                                                                                                                                                                          PAKI_HUMAN STANDARD; PRT; 545 AA.

013153; Q13567;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-)
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75
DOMAIN 75
DOMAIN 134
DOMAIN 269
NP_BIND 275
NP_BIND 275
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     SEQUENCE FROM N.A
                                                  NCBI_TaxID=9606;
                                                                           Mammalia;
                                                                                               Eukaryota; Metazoa;
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SMART; SM00220; S_TKC; 1.
PROSITE; PS50108; CRIB; 1
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EMBL; U49953; AAB615;
PIR; S40482; S40482.
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InterPro; IPR000095; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
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                                                                                                                           sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                           FLNRCLEMDVEKRGSAKELLQHQFLKIAKPLSSLTPLIAAAKEATK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00107;
                                                                           Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equires a license agreement (See http://www.isb-sib.ch/announce/
email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              544 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB95646.1;
AAB61533.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRIB; 1.
PROTEIN KINASE ATP; 1.
PROTEIN KINASE ST; 1.
PROTEIN KINASE ST; 1.
Companies of the protein kinase; ATP-binding;
                                                                                                                                                                        (P65-PAK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268
520
283
298
388
                                                                           Primates;
                                                                                             Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60577 MW;
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                                                                                                                                                                     (Alpha-PAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 510; DB 1;
Pred. No. 4.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRIB.
                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93BE32D8222F5B7B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                          (p21-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by and for
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tent is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            commercial
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В
                      20
                                                                                               Query Match
Best Local S
Matches 117
                                                                                                                                                                                                                                                                           SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN,
PROSITE; PS50011; PROTEIN
                                                                                                                   Phosphorylation.
DOMAIN 75
DOMAIN 134
DOMAIN 270
NP_BIND 276
BINDING 299
ACT_SITE 389
ACT_SITE 389
ACT_SITE 379
CONFLICT 237
CONFLICT 379
                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                             MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U24152; AAA65441.1; -. EMBL; U51120; AAC50590.1; -. HSSP; P24941; 1CKP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The Buropean Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human Ste20 homologue hPAK1 links GTPases pathway.";
                                                                                                                                                                                                                                                      Transferase;
                                                                                                                                                                                                                                                                  PROSITE; PS00108;
                                                                                                                                                                                                                                                                                                                                       ProDom;
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00095; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC:8590; PAK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: THE ACTIVATED KINASE ACTS ON A VAR-
LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS
GTPASES TO THE JNK MAP KINASE PATHWAY.
-!- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BU
CDC42/P21 AND RAC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammalian cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 CRIB DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96398842; PubMed=8805275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chernoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97199447; PubMed-9395435;
Sells M.A., Knaus U.G., Bagrodia S., Ambrose D.M.,
  265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human p21-activated kinase (Pakl) regulates actin organization
                       23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STE20 SUBFAMILY.
                DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL--
                                                                                                                                                                                                                                                                                                                                                                                                             602590;
                                                al Similarity
117; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. 6:598-605(1996).
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                                                                                               545
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7:202-210(1997)
                                                                                                                                                                                                                                                      Serine/threonine-protein
                                                                                               AA;
                                                                                                                                                                                                                                                               PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                      PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                       Euk_pkinase;
                                                                                                                     88
269
521
521
284
299
389
107
26
237
379
                                                                                             60661 MW;
                                                          30.3%;
                                                51;
                                                                                                       ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY
L->F: CONSTITUTIVELY A
V -> A (IN REF. 2).
R -> L (IN REF. 2).
F -> S (IN REF. 2).
D -> E (IN REF. 2).
                                                          Score 508; DB 1;
Pred. No. 5.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Bioinformatics
                                                                                                                                                                                                       PROTEIN KINASE
                                                                                                                                                                                                                    LINKER.
                                                                                              14A1E70E6480CD7E CRC64;
                                               Mismatches
                                                                                                                                                                                                                                                     kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ON A VARIETY OF TARGETS
AT LINKS THE RHO-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ťo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDC42/P21.
OF PROTEIN KINASES
-QQQPKKELIINEILVMRE 321
                                                                   Length 545;
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                                               Indels
                                                                                                                                                         ACTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collaboration
                                              Gaps
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LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141

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RESULT 9
PAKI_MOUSE
ID PAKI_M
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DT 15-DEC
DT 15-
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                   SMART; SM00285; PBD; 1.
SMART; SM00220; S.TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATD;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
                                                                                                                                                                                                                                    MGD; MGI:1339975; Pakl.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000995; Pakbox/Rhobndng.
InterPro; IPR00299; Ser thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a control between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-)
kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK) (CDC42/RAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, central nervous the mouse PAK-1 and PAK-3 Gene 232:209-215(1999).
                                                                                                                                                                                                           Pfam; PF00069; pkinase; 1 Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse Eukaryota; Metazoa;
     Transferase;
                                                                                                                                                                                     ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99282526; PubMed=10352232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAK1 OR PAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 1 CRIB DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                     P24941; 1CKP
                                                                                                                                                                                                                                                                                                                                                                                                   AF082077; AAC32375.1; -.
                                                                                                                                                                                  PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
  Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      runegold A.A., Hall A., Pirone D.I system expression and chromosomal genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE SER/THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHEN ACTIVATED BY CDC42/P21 (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAMILY
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ATP-binding;
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Murinae; Mus
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Best Local
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PAT
                                                                                                                                                                                                                                                                         Kinase (pak) family,";

J. Biol. Chem. 270:25070-25078(1995).

J. Biol. Chem. 270:25070-25078 (1995).

J. Biol. Chem. 270:25078 
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DOWAIN 75
DOWAIN 134
DOWAIN 270
MP_BIND 276
BINDING 299
ACT_SITE 389
SEQUENCE 545 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q62829;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Serine/threonine-protein kinase PAK 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
NP_BIND
BINDING
ACT_SITE
SEQUENCE
This SWI
between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
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                                                                                                                                                 DOMAINS OF PHOSPHOLIPASE C-GAM
SIMILARITY).

SIMILARITY).

1- TISSUE SPECIFICITY: DETECTED A:

LOW LEVELS IN THE TESTIS.

1- DEVELOPMENTAL STAGE: FOUND IN :

EXPRESSION ELSEWHERE.

1- PIM: AUTOPHOSPHORYLATED WHEN A:

1- PIM: AUTOPHOSPHORYLATED WH
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nes 116; Conserv
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                                                                            STE20 SUBFAMILY.
SIMILARITY: CON'
                                                                                                                                SIMILARITY:
                              SWISS-PROT
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    (PAK-3) (Beta-PAK) (P65-PAK).

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chong
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ROT entry is copyright. It is prod
Swiss Institute of Bioinformatics
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                                                                            CONTAINS 1
                                                                                                                                BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                С.,
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C., Zhao Z.~S.,
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                                                                            CRIB DOMAIN
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ATP (BY SIMILARITY).
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LINKER.
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Sciurognathi; Muridae
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(EC 2.7.1.-)
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                     produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 116
                                                                                         075914;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 3 (EC 2.7.)
Kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phosphorylation.
DOMAIN 10
DOMAIN 1268
DOMAIN 268
NP_BIND 274
BINDING 297
ACT_SITE 387
SEQUENCE 544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
 MEDLINE=98400251; Pallen K.M., Gleeson
                                                                 Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                          SEQUENCE FROM N.A.
                                                 Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                        Homo sapiens (Human)
                                                                                                                                                                                               PAK3_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR00095; PAKDOX/AUGUAL,
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Euk_pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                              495
                                                                                                                                                                                                                                                                                        257
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLNRCLEMDVDRRGSAKELLQHPFLKLAKPLSSLTPLILAAKEAIK 540
                                                                                                                                                                                                                                                                                                                             DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEYFRN
                                                                                                                                                                                                                                                                                                                                                                                LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                     NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                     FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR
                                                                                                                                                                                                                                                                                                             {\tt TRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQNPERLSAVFRD}
                                                                                                                                                                                                                                                                                                                                                                LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P24941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U33314; AAC52268.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50011; PROTEIN_KINASE_DOM; 1 PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000719;
                                                                             Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1CKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α̈́A,
                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
267
519
282
297
387
60710 :
             PubMed=9731525
                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.1%;
 .G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euk_pkinase.
 Bagrodia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKER.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 505;
Pred. No. 9
                                                                Craniata; Vo
Catarrhini;
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7B940FC204A2B48B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
s.
                                                                                                                                                                                              544
Partington
                                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
.9e-31;
                                                                                                                                                                                              ΑA
                                                                 Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 544;
 M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                            (p21-activated
                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                           197
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                                                                                                                                                                                                                                                                                                                                                                  434
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Matches 116
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                                                                                                                                                                                                                                                           ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; PBD; 1.
SMART; SM00220; STKC; 1.
SMART; SM00220; STKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and i
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069;
Pfam; PF00786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF068864; AAC36097.1; HSSP; P24941; 1CKP.
                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                   SH3-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
495
                     257
                                          435
                                                               198
                                                                                   378
                                                                                                        142
                                                                                                                              320
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                                                                                                                                                 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STE20 SUBFAMILY
                                                                                                                          NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALDF
                                                                                                                                                                                       DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
                                                    DEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEYFRN
                                                                                             LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                         300142
FLNRCLEMDVDRRGSAKELLQHPFLKLAKPLSSLTPLIIAAKEAIK
                  FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR
                                        TRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQNPERLSAVFRD
                                                                                  LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                      DPKKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC:8592; PAK3.
                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000719; Euk_pkinase.
IPR000095; PAKbox/Rhobr
IPR002290; Ser_thr_pkir
                                                                                                                                                                                                                                                       387
544
                                                                                                                                                                                                                                                                          70 83 129 267 16
268 519 27
274 282 27
297 297 1
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                PBD;
                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                           pkinase; 1.
                                                                                                                                                                                                                                                        267
519
282
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297
387
60692
                                                                                                                                                                                                                        30.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAKbox/Rhobndng
                                                                                                                                                                                                                                                            W.
                                                                                                                                                                                                                52;
                                                                                                                                                                                                              Score 504; DB Pred. No. 1.2e 52; Mismatches
                                                                                                                                                                                                                                                                 LINKER.

PROTEIN KINASE.

PROTEIN (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                           CRIB
                                                                                                                                                                                                                                                           230AF6952CB049E2 CRC64;
                                                                                                                                                                                                                                                                                                                                              kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  moved. Usage by and for (See http://www.isb-sib.
                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                      -QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                   Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
                                                                                                                                                                                                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
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RESULT 12
PAK3_MOUSE
       TATE TO CONSON OF THE PROPERTY OF A PROPERTY OF THE PROPERTY O
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HSSP; P24941; Ich...
MGD; MGI:1339656; Pak3.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000095; PaKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
ThterPro; Oraconnkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q61036; O88645;

O1-NOV-1997 (Rel. 35, Created)

O1-NOV-1997 (Rel. 35, Last sequence update)

O1-JUN-2002 (Rel. 41, Last annotation update)

Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated kinase 3) (PAK-3) (Beta-PAK) (CDC42/RAC effector kinase PAK-B).
                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fibroblast;
MEDLINE=96032693; PubMed=7559398;
MEDDINE=96032693; PubMed=7559398;
MEDDINE=960326939; PubMed=960326939; PubMed=9603269
                                                                                                                                                                                                                                     SMART; SM00220; S_TKC; 1.

PROSITE; PS50108; CRIS; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP;

PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ish-aih ah)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99282526; PubMed=10352232; Burbelo P.D., Kozak C.A., Finegold A.A., Hall A. "Cloning, central nervous system expression and the mouse PAK-1 and PAK-3 genes.";
                                                                                                                                    Transferase;
SH3-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 232:209-215(1999).
       NP_BIND
                                                                                                           DOMAIN
                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00285; PBD;
                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39738; AAC52354.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bagrodia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERRATUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAK3 OR PAK-3 OR STK4 OR PAKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAK3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CDC42/P21 AND RAC1. SHOWS HIGHLY SPBCIFIC BINDING TO THE SH3
DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 CRIB DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF082297;
                                                                                                                                                                                                                                                                                                                                                                                                                    PD000001; Euk_pkinase;
                                                                                                                                                                                                               PS00108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S., T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
); Phosphorylation.
70 83 C
129 267 L
268 519 P
274 282 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taylor S.J., Creasy C.L., n. 271:1250-1250(1996).
                                                                                                                                                                        Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC31969.1; -.
                                                                                                                                                                                                               PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Rodentia;
LINKER.
PROTEIN
ATP (BY
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Sciurognathi;
KINASE.
SIMILARITY).
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                                                                                                                                                                        kinase;
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thi; Muridae;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cerione
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Best Local
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ACT_SITE
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine-protein kinase 10 (EC 2.7.1.37) (Lymphocyte-oriented
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                 HISTONE IIA ON SERINE AND THREONINE RESIDUES
-:- CATALYTIC ACTIVITY: ATP + a protein = ADP + a
-:- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY:
                                                                                                                                                                                                                                                                                                                                                                                                                      ST10_MOUSE
055098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                - -
                                                                                                                                                                                                J. Biol.
                                                                                                                                                                                                       predominantly in
                                                                                                                                                                                                                                          MEDLINE=97426413; PubMed=9278426;
Kuramochi S., Moriguchi T., Kuida K.,
                                                                                                                                                                                                                                                                    TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                     STK10
                                                                                                                                                                                                                                                                                                                                                              kinase)
                                                                 between
                                                                              This
                                                                                                                                                                                     -
                                                                                                                                                                                                                                  Karasuyama H.;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                    "LOK is a novel mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                 K is a novel mouse STE20-like prot
dominantly in lymphocytes.;
Biol. Chem. 272:25679-25684(1997).
FUNCTION: CAN ACT ON SUBSTRATES S
                                                                                                               PTM: AUTOPHOSPHORYLATED. SIMILARITY: BELONGS TO T
                                                                                                                                      SUCH AS SPLEEN, THYMUS, AND BONE MARROW
                                                                                                     STE20 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVR 302
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G -> A (IN I
V -> E (IN I
H -> R (IN I
L -> M (IN I
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                               SER/THR FAMILY
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2.4e-30;
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                                                                  a collaboration -
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SPS1_YEAST
ID SPS1_Y
AC P08458
AC P08458
DT 01-AUG
DT 01-NOV
DT 30-MXY
DE SPOTUL
GN SACCHA
OC EUKATY
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P08458;
01-AUG-1988 (Rel. 08, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Sporulation-specific protein 1 (EC 2.7.1.-).
SPSI_OR YDR523C OR D9719.27.
                          Dietrich F.S., Mulligan J., Allen E., Araujo R., A
Berno A., Carpenter J., Chen E., Cherry J.M., Chur
Hunicke Smith S., Hyman R., Komp C., Lashkari D.,
Mosedale D., Nakahara K., Namath A., Oefner P., Oh
Roberts D., Schramm S., Schroeder M., Shogren T.,
Winant A., Yelton M., Botstein D., Davis R.W.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                             Submitted (AUG-1994)
                                                                                                                                                                                                                                                                                                                           Friesen
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Coiled coil.

Domain 36 294 PROTEIN KINASE.

DOMAIN 588 936 COILED COIL (POTENTIAL).

DOMAIN 749 883 COILED COIL (POTENTIAL).

DOMAIN 749 883 GLN-RICH.

NP_BIND 42 50 ATP (BY SIMILARITY).

BINDING 65 65 ATP (BY SIMILARITY).

ACT_SITE 157 157 BY SIMILARITY.

SEQUENCE 966 AA; 111992 MW; 7115EACO1032BF94 CRC64;
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
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                                                                                                                                           Chung E., Duncan
D., Lew H., Lin [
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                                                                                                                                                                                                    Aviles E.,
                                                                                      h C., Petel F.X.,
Shroff N.,
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PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
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SMART; SM00220; S_TKC; 1.
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U13018; AAA64833.1; -. EMBL; U33057; AAB64963.1; -. EMBL; M13629; AAA35079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cerevisiae.";
Mol. Cell. Biol. 6:2443-2451(1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87064542; PubMed=3023934;
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SIMILARITY: BELONGS
STE20 SUBFAMILY.
KYPLQ
                                              KILFQ
                                                                                                                     DSCLQKIPQDRPTSEVLLKHRFVLRERPPTVI-----MDLIQRTKDAVRELDNLQYRKMK 313
                                                                                                                                                                                                             в25376; в25376.
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                                                                                                                                                                                     DG-YNEKADIWSLGITTYELLKGLPPLSKYDPMKVMTNLPKRKPPKLQ-GPFSDAAKDFV
                                                                                                                                                                                                                                                                                  LHEQRKIHRDIKAANILLNEEGMVKLGDFGVSGHIRSTLKRDTFVGTPYWMAPEVVCCEV
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                                                                                                                                                                                                                                                                                                                                                                               KSPLITNYIATMLEDVSMWIVMEYCGGGSCSDLLKRSYVNGLPEEKVSFIIHEVTLGLKY
                                                                                                                                                                                                                                                                                                                                                                                                                           RHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLE-VHKKPLQEVEIAAVTHGALQGLAY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSKLYSIQSCIGRGNFGDVYKAVDRVTQEIVAIKVVNL--EHSDEDIELLAQEIFFLAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQKL 83
                                                                                          AGCLVKTPADRPSAYNLLSFEFV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125;
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ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND HISTONE IIA ON SERINE AND THREONIRE RESIDUES (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS.
-!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
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Homo sapiens (Human).
'arvota; Metazoa; Chordata; '
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                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0109; TYRKINASE.

PRODOM: PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Kurasuyama H.;
Molecular cloning of the human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB015718; BAA35073.1; -. EMBL; AL133081; CAB61400.1; -. HSSP; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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         Conservative
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                                   le-29;
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      112;
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FRDFLKTALDKNPETRPSAAQLLEHPFVSSITSNKALRELVAEAKAEVME
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Search completed: November 22, 2002, 12:24:14 Job time: 6.96 secs

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               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compugen Ltd
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serine/threoine pr
serine/threonine-s
p21-activated prot
protein kinase SK2
serine/threonine p
beta-p21-activated
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protein kinase, p2
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Qy Db	ОУ	Оу	Оу	ОУ	Qy Db	Que Bes Mat	RESUI T1733 Serih C; Sp C; Sp C; Ac C; Ac C; Ac A; Ti A; Re A; Ts A; Re A; Re C; Ac C; Ac	
301 V	241 E 241 E	181 S	121 K 121 K	61 Y 61 Y	x – x	ery Match st Local S: tches 284	RESULT 1 T17365 serine/threonine protein kins serine/threonine protein kins cycles (). Species: Rattus norvegicus (). Species: Rattus norvegicus (). Date: 15-Oct-1999 #sequence (). Accession: T17365 R; Hutchison, M.; Berman, K.S. J. Biol. Chem. 273, 28625-288 A; Fittle: Isolation of TAO1; A.; Reference number: Z18730; A.; Reference number: Z18730; A.; Accession: T17365 A; Status: preliminary; transl A; Molecule type: mRNA A; Residues: 1-1001 <hut> A; Cross-references: EMBL: AF08 C; Function: probably impli</hut>	1 4 4 3 4 3 4 4 3 4 4 4 3 4 4 4 3 4 4 4 4 3 4 4 4 4 3 4 4 4 4 3 4
RELDNL	SPALQS	FVGTPY       FVGTPY	PLQEVE        PLQEVE	SGKQSN       SGKQST	PAGGRA  :     PSTNRA	`` ∄	threonine es: Rattus 15-Oct-19 sion: T173 iison, M.; Chem. 27 i: Isolatio ence numbe ence numbe sis: prelimi ule type: lues: 1-100 in: in:	44444 01111334 01111155
QYRKMK 	SGHWSEYFRNFVDSCL	WMAPEV        WMAPEV	IAAVTH    :   IAAITH	EKWQDI        EKWQDI	GSLKDP       GSLKDP	ilarity Conservat	eonine protein kinası Rattus norvegicus () -Oct-1999 #sequence) n: T17365 nn, M.; Berman, K.S.; hhem. 273, 28625-28631 solation of TAO1, a 1 se number: Z18730; MU preliminary; transla; type: mRNA; 1-1001 <hut> tferences: EMBL:AF084; ion: probably implic:</hut>	22226.2 2225.0 22225.0 22225.0 22225.0 22226.0 22226.0 222
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320	SCLOKIPODRPTSEVLKHREVLRERPPTVIMDLIQRTKDA 	FVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMS 	KPLQEVETAAVTHGALQGLAYLHSHNMTHRDVKAGNILLSEPGLVKLGDEGSASIMAPAN 	SGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGGYLREHTAWLVWEYCLGSASDLLEVH 	MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS   :       ::	Score 1529; DB 2; Length Pred. No. 2.7e-68; 22; Mismatches 14; Indels	ADD - rat  ADD - rat  way rat) ision 15-Oct-1999 #text. bb, M.H. 1998 1998 1998 19903202; PMID:9786855 from GB/EMBL/DDBJ ; NID:g3452472; PID:g344 d in the regulation of :	
	'IMDLIQRTKDA 300 ::         /LIDLIQRTKDA 300	AMSALYHIAQN 240             AMSALYHIAQN 240	)FGSASIMAPAN 180      : :     FGSASMASPAN 180	GSASDLLEVHK 120            GSASDLLEVHK 120	RNSEVVAIKKMS 60 	h 1001; els 0; Gaps	_change 15-Oct-1999 tes MEKs in stress-activate tes pidn:AAC71014.1 the p38-containing stress-r	probable serine/th protein kinase-lik serine/threonine-p hypothetical prote hypothetical prote protein kinase Pak probable MEK kinas hypothetical prote hypothetical prote probable protein k hypothetical prote protein kinase CLA hypothetical prote protein kinase CLA hypothetical prote hypothetical prote protein kinase CLA hypothetical prote hypothetical prote hypothetical prote

serine-threonine kinase - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

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C; Date: Verman, C; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Caccession: B96716
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A; Authors: Hunter, J.L.; Jenkins, S.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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B96716
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A;Molecule type: mRNA
A;Residues: 1-982 <BAR>
A;Cross references: EMBL:U32275; E
A;Experimental source: strain N2 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable serine/threonine kinase F23010.20 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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R; Cope, M.J.T.V.; Kend
submitted to the EMBL
                                                                                                                  C; Genetics
                                                                                                                                                         A; Residues: 1-836 <STO>
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al Similarity
127; Conserv
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57.9%;
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47
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                  . 28;
54;
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                                                                                                                                    NID: 97705100; PIDN: AAF67779.1;
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                Score 631.5;
Pred. No. 2.0
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                                    836;
11;
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hypothetical protein T19A5.2 - Caenorhabditis elegans C;SpecLes: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #tC;Accession: T34356

#text\_change

29-Oct-1999

R;Bradshaw, H

submitted to the

EMBL

Data

Library,

March 1996

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T34356
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A; Residues: 1-426 < PONE.
A; Cross-references: EMBL: X99325; NID:91430821; PIDN:CAA67700.1;
A; Experimental source: cell type B cell
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase
C; Keywords: ATP; autophosphorylation; phosphotransferase; protei
C; Keywords: ATP; autophosphorylation; phosphotransferase; protei
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C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change
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R;Pombo, C.M.; Bonventre, J.V.; Molnar, A.; Kyriakis, J.; Force, T. EMBO J. 15, 4537-4546, 1996
A;Title: Activation of a human Ste20-like kinase by oxidant stress A;Reference number: S71886; MUID:97042345; PMID:8887545
A;Accession: S71886
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                                                                                                                                                              LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSEVGTPYWMAPEVILAM
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                                                                                                                                                                                                                                                                                                                                                                DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ 72
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                                                                     VEACLNKDPRFRPTAKELLKHKFITRYTKKTSFLTELIDRYK
                                                                                                                                             KQSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKNSPPTLEGQH-SKPFKEF
                                                                                                                                                                                                                  LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNEVDSCLQKIPQDRPTSEVLLKHREVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --QENRYDGKVDVWALGVSAIEMAEGLPPRSSVHPMRVLFMISIEPAPMLEDKEKWSLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSAS----IMAPANSFVGTPYWMAPEVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVADLMNVTEEALEEYQIAYICREALKGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 576; DB 2;
Pred. No. 8.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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submitted to the EMBL Data Library, April 1996
A; Description: The sequence of C. elegans cosmid ZC404.
A; Reference number: Z20614
A; Reference number: Z20614
A; Recession: T29372
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-829 <BEN>
A; Cross-references: EMBL:U55363; PIDN:AAA97966.1; GSPDB:GN00023; CESP:Z
A; Experimental source: strain Bristol N2; clone ZC404
C; Genetics:
A; Gene: CESP:ZC404.9
A; Map position: 5
A; Introns: 36/2; 82/2; 103/1; 131/3; 520/3; 622/2; 796/2
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: The sequence of C. elegans cosmid T19A5.
A; Reference number: Z21512
A; Accession: T34356
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-653 <BRA>
A; Cross-references: EMBL:U53153; PIDN:AAC69038.1; GSPDB:GN00023; CESP:T19A5.
A; Experimental source: strain Bristol N2; clone T19A5
C:Genetics:
A; Genetics:
A; Genetics:
A; Gene: CESP:T19A5.2
A; Map position: 5
A; Introns: 26/3; 101/3; 157/1; 209/3; 272/3; 305/2; 373/3; 635/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein ZC404.9 - Caenorhabditis elegans
(;Speciles: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T29372
R;Bentley, D.; Le, T.T.
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                                                                                                                                                                                                                                   Local
                                                                                                                                                                      AELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFVEMCLNKDPENRPSASTLLKHQFIKRAKKNSILVDLIERAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKD 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EYLHSERKIHRDIKAANVLVSEHGDVKVADFGVAGQLTETVKKRITFVGSPFWMAPELI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLDPEVIFTKQERIGRGSFGEVYKGIDNRTGRVVAIKIIDL--EQAEDEIEDIQQEIQVL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFL
          ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAPANSFVGTPYWMA 190
                                                  EIMVIRECSHPNIIAYFGSYIRRDRLWIVMEYCGGGSLQDIYHL-TGPLSELQIAFVCRE 118
                                                                                        EVRELOKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHG 134
                                                                                                                                ADVIKRSNPADDYELLQRVGSGTYGEVYKARDIRSDSLAAVKVVKL---EAGDNFAVIQQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --KQSSYDYKADIWSLGITAIELANGEPPHSDLHPMRVLFLIPKNPPPVLQGSQWSKPFK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQCDSQYVTKYFGSFLKGSKLWIIMEYLGGGSALDLTKSGK--LDESHIAVILREILKGL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120;
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                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 565; DB 2; Pred. No. 4.1e-21;
                                                                                                                                                                                                                                 Score 541.5; DB 2; Pred. No. 7.2e-20;
                                                                                                                                                                                                                  Mismatches
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A;Reference number: Z23032
A;Accession: T46444
A;Status: preliminary
                                                                   C;Accession: T46444
R;Bloecker, H.; Boecher, M.;
submitted to the Protein Sequence
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C; Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Sep-1999 (C; Accession: A53714 R; Katz, P.; Whalen, G.; Kehrl, J.H. J. Biol. Chem. 269, 16802-16809, 1994 A; Title: Differential expression of a novel protein kinase in human B lympho A; Reference number: A53714; MUID:94266900; PMID:7515885 A; Accession: A53714 A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-819 < KAT> A; Cross-references: GB:U07349; NID:9531819; PIDN:AAA20968.1; PID:9531820 C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein )
hypothetical protein DKFZp434N1427.1 - human
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: unassigned Ser/Thr or Tyr-specific C;Keywords: ATP; phosphotransferase F;13-272/Domain: protein kinase homology <KIN>F;21-29/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Alternate names: GC kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase (EC 2.7.1.37) BL44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                     NEHHFLKLALTKNPKKRPTAEKLLQHPFTTQQLPRALLTQLLDKASD
                                                                                                                                                                                             YFRNFVDSCLQKIPQDRPTSEVLLKHRFVLKERPPTVIMDLIQRTKD
                                                                                                                                                                                                                                                                                                                                                           HLHSQGKIHRDIKGANLLLTLQGDVKLADFGVSGELTASV-AKRRSFIGTPYWMAPEVAA 183
                                                                                                                                                                                                                                                                                                                                                                                                          YLHSHNMIHRDVKAGNILLSEPGLVKLGDFG-----SASIMAPANSFVGTPYWMAPEVIL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRHPNVVAYIGSYLRNDRLWICMEFCGGGS--LQEIYHATGPLEERQIAYVCRERLKGLH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPRDRFELLQRVGAGTYGDVYKARDTVTSELAAVKIVKL---DPGDDISSLQQEITILRE
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                                                                                                                                                                                                                                                                   VERKGGYNELCDVWALGITAIELGELQPPLFHLHPMRALMLMSKSSFQPPKLRDKTRWTQ
                                                                                                                                                                                                                                                                                         AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN--ESPALQ-SGHWSE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEVACVEKRGGYGMQCDVWATGITAIELGECQPPLFDLHPMQVLYLMTKSGYKPPHLKDK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN--ESPALQSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.6%; Score 530; DB 2;
40.1%; Pred. No. 2.6e-19;
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5; Mismatches
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Brandt, P.;

Mewes, H.W.; January

; Gassenhuber, 2000

Wiemann,

ß

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RESULT 10
JC6316
                   probable protein kinase (EC 2.7.1.-) -
C;Species: Drosophila melanogaster
C;Date: 21-May-1999 #sequence_revision
C;Accession: JC6316
                                                                                                                                                                                                                                                                                 δõ
                                                                                                                                                                                                                                                                                                                             DЬ
                                                                                                                                                                                                                                                                                                                                                              Qy
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A;Molecule type: mRNA
A;Residues: 1-1233 <SUY>
A;Cross-references: EMBL:UB8984; NID:g1872545; PID:g1872546; PIDN:AAC53165.1
C;Keywords: protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Su, Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y. EMBO J. 16, 1279-1290, 1997
A;Title: NIK is a new Ste20-related kinase that binds NCK A;Reference number: Z20954; MUID:97280817; PMID:9135144
A;Accession: T30989
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A:Residues: 1-1062 cANA>
A:Cross-references: EMBL:AL137701
A:Experimental source: adult testis; clone DKFZp434N1427
C:Genetics:
A:Note: DKFZp434N1427.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: Nck interacting kinase
C;Speciles: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T30989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                     MSALYHIAQNESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERP----
                                                                                                                                                                         VRIQLKDHIDRTRKKRGEKDETEY
                                                                                                                                                                                                                                                                                                                                                --MAPANSFVGTPYWMAPEVILAMDE---GQYDGKVDVWSLGITCIELAERKPPLFNMNA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKSLVDIDLSSL---RDPAGIFELVEVVGNGTYGQVYKGRHVK-TVTAAIKVMDV----T 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRFVLRERPPTVIMDLIQRTKDAVRELDNLQYRKMKKILFQEA
                                                                                                                                                                                                              -PTVIMDLIQRTKDAVRELDNLQY 309
                                                                                                                                                                                                                                                                                                                             RTVGRRNTFIGTPYWMAPEVI-ACDENPDATYDYRSDLWSCGITAIEMAEGGPPLCDMHP
                                                                                                                                                                                                                                                                                                                                                                                                   TKGNTLKEDWIAYISREILRGLAHLHIHHVIHRDIKGQNVLLTENAEVKLVDFGVSAQLD 178
                                                                                                                                                                                                                                                                                                                                                                                                                           HK-KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFG-SASI- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131;
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                                                                                                                                                                                                                                                  MRALFLIPRNPPPRLKSKKWSKKFFSFIEGCLVKNYMQRPSTEQLLKHPFI-RDQPNERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDEEEEITLEINMLKKYSHHRNIATYYGAFIKKSPPGHDDQLWLVMEFCGAGSITDLVKN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEKWQDIIKEVRFLQKL-RHPNTIQYRGCYLR-----EHTAWLVMEYC-LGSASDLLEV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 528; DB 2; Pred. No. 4.1e-19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                         21-May-1999 #text_change 21-May-1999
                                                                            fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7e-19;
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C9572
                                                                                                                                                                                                                                                                                                                                               R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, (Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hujbas, B.; Hulzar, L.
Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: msn
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Experimental source: third instar eye-ai A;Note: the cited accession number, 10764
A;Map
                                       C; Genetics:
                                                                  A; Cross-references:
                                                                                      A; Molecule type: DNA
A; Residues: 1-690 <STO>
                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein F12M16.4 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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Best Local S
Matches 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEKEREDYR 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELDNLQYR 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APEVILAMDE---GQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQ 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSNHRNIATYYGAFIKKSPPGKDDQLWLVMEYCGAGSVTDLVKSTKGQSLKEEWIAYICR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L-RHPNTIQYRGCYL-----REHTAWLVMEYC-LGSASDLLEVHK-KPLQEVEIAAVTH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKKWSKKFHGFIDTVLVKDYHQRPYTENLLKHGFI-KDQPTDRQVRIQLKDHIDRCKKRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPP----TVIMDLIQRTKDAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APEVI-ACDENPDATYDNRSDLWSLGITALEMAESQPPLCDLHPMRALFLIPRNSPPRLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                             GB:AE005173; NID:g7769851; PIDN:AAF69529.1;
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                                                                  GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                           Khaykin,
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Query Match Best Local Matches 12

Local Similarity

31.2%;

Score 523; DB 2 Pred. No. 5e-19;

2;

Length 690;

Conservative

48;

Mismatches

98;

Indels

22;

Gaps

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A;Residues: 1-1
A;Cross-referen
A;Experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine/threoine protein kinase - guinea pig
N;Alternate names: STE20-like kinase
C;Species: Cavia porcellus (guinea pig)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_ch
C;Accession: T18532
R;Itoh, S.; Kameda, Y.; Yamada, E.; Tsujikawa, K.; Mimura,
serine/threonine-specific protein kinase (EC 2.7.1.-) -
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text
                                                  RESULT
S40482
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A;Title: Molecular cloning and characterization of a novel putative STE20-like kinase A;Reference number: Z18952; MUID:97288344; PMID:9143322
A;Accession: T18532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Matches
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;Residues: 1-1231 <ITO>
;Cross-references: EMBL:D88425; NID:g2911113; PIDN:BAA24930.1;
;Experimental source: strain Hartley; liver
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                                                                                                                                                                                                                    IAQNESPAL-QSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFV-LRERPPTVIMDLI 294
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Pred. No. 3.4e-18;
7; Mismatches 116;
 #text_change
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p21-activated protein kinase - C;Species: Homo sacion-
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C; Accession:
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                                                                                                                                                                                                                                                                                                        A;Gene: Pak1
C;Superfamily: unassigned
F;268-521/Domain: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: G01773
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A;Title: A brain serine/threonine
A;Reference number: S40482; MUID:9
A;Accession: S40482
                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-545 < CHE>
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A; Residues: 1-544 <MAN>
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R; Manser, E.; Leung,
                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: U24152;
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDB:
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21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
sion:_G01773
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                       LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM 197
                                                                                             FVDSCLQKIPQDRPTSEVLLKHREVLRERPPTVIMDLIQRTKDAVR 302
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                                                                                                                                                   DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE 321
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D-46, 1994
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kinase homology <KIN>
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Pred. No. 1.8e-18;
2; Mismatches 10;
                                                                                                                                                                                                                             Score 508; DB 2;
Pred. No. 2.2e-18;
1; Mismatches 104
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R;Fukami, Y.; Yamamoto, H.; Ichihara, T.; Mori, K.; Gomi, T.; Sato, K. submitted to the EMEL Data Library, April 1997
A;Description: SK2, a putative rat homologue of yeast protein kinase NRK1.
A;Reference number: Z21463
A;Accession: T34021
Search completed: November 22, 2002, 12:27:19 Job time: 13.96 secs
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A;Molecule type: mRNA
A;Residues; 1-1206 <PUK>
A;Cross-references: EMBL:AB003357; NID:d1106513; PID:d1020890; PIDN:BAA20077.1
A;Experimental source: strain SD
C;Genetics:
A;Gene: SK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein kinase SK2 - rat
C;Specles: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34021
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Best Local Similarity
Matches 118; Conserv
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                                                                                                                                                                                                                                                                             LTESQIQVVCKQTLEALNYLHDNKIIHRDLKAGNILFTLDGDIKLADFGVSAKNTRTIQR 186
                                                                                                                                                                                                                                                                                                 LQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFG----SASIMAP 178
                                                                                                                                      IAKSEPPTLAQPSRWSSNFKDFLKKCLEKNVDARWTTSQLLQHPFVTVDSNKP---VREL 303
                                                                                                                                                            IAQNESPAL-QSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVL--RERPPTVIMDL 293
                                                                                                                                                                                                                                                                                                                                                                      QSNEKWQDIIKEVRFLQKLRHDNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKF 122
                                                                                                       IQRTKDAVRE 303
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Minimum DB
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      Score
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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US-09-48-442-3
US-09-185-370-2
US-09-185-370-2
US-09-185-370-9
US-09-111-444-8
US-09-211-930-3
US-09-211-930-3
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RESULT 1 US-09-060-410-4 ; Sequence 4, A ; Patent No. 61 ; GENERAL INFO ; APPLICANT:		45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	
		487.5	489	489	491	491	491	491	491	491	491	497	499	503	503	505	516	516	550	
Application US/C 6165461 FORMATION:		29.1	29.1	29.1						•	29.3			•			•	30.8		
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50410	ALIGNMENTS	US-08-852-743-6	US-09-185-370-3	US-08-852-743-3	US-08-615-942A-2	-262-	-509-	US-08-636-036-2	US-08-780-833-2	US-08-475-682-2	US-08-369-780-2	US-08-559-397A-19	US-08-559-397A-2	US-08-935-760-2	US-08-114-555A-2	US-08-935-760-4	US-09-185-370-7	US-08-852-743-7	US-09-541-228-3	·
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                                                        Query Match
Best Local Similarity
Matches 320; Conserv
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
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CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                      LENGTH: 993 amino acids TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS 60
MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
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                                                                    Conservative
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                                                                                   100.0%; Score 1678; DB 4; 100.0%; Pred. No. 4.7e-157;
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                                                                Matches
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                                                                                                                                                                                                          TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BETMAN, KEVIN
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 26
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APPLICANT:
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                                                                                                                                                              LENGTH: 1001 amino acids TYPE: amino acid TOPOLOGY: linear
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             1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS 60
MPSTNRAGSLKDPEIAELFFKEDPEKLFTDLREIGHGSFGAVYFARDVRTNEVVAIKKMS 60
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Pred. No. 2.5e-142;
22; Mismatches 14;
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                                                                                                 Query Match
Best Local Similarity
Matches 162; Conserv
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Patent No. 6165461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: DOUG
STREET: Seattle
CTATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: TAO F
TITLE OF INVENTION: THERE
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66
                                                                                                                                                                                                  TYPE: amino STRANDEDNESS:
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SNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQE 125
                                 KPGVIKDPSIAALFSNKDPEQ----DLREIGHGSFGAVYFAYDKKNEQTVAIKKMNFSGKQ 64
                                                                RAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQ 65
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                                                                                               52.1%; score 873.5; llarity 59.1%; Pred. No. 2.26 Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                      (206)
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                                                                                                                                                                                    Linear
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US-09-211-930-5
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Sequence 5, Application US/09340993
Patent No. 6034228
GENERAL INFORMATION:
APPLICANT: Tyrell E. No. 6034228ris
APPLICANT: William Craiq Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
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EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 5
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Best Local Similarity
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Patent No. 5962265
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APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 431
TYPE: PRT
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                                                                                                                                                                                                                                                                                                         AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFR 255
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APPLICANT: Tyrell E. No. 6265560ris
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN STE20-LIKE STRESS ACTITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70272
CURRENT APPLICATION NUMBER: US/09/152,406
CURRENT FILLING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: 9719920.2
EARLIER APPLICATION NUMBER: 9719920.2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-993-5
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
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Patent No. 6265560
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                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                    Matches
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CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930
EARLIER FILING DATE: 1997-12-19 & 1998-12-15
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 EFVEACLNKEPSFRPTAKELLKHKFILRNAKKTSYLTELIDRYK 292
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                                                                                                        KDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAIKIIDL--EEAEDEIEDIQQEITVL 74
                                       QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE---PGPLDETQIATILREILKGL 132
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SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL 132
                                                                                KADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAIKIIDL--EEAEDEIEDIQQEITVL 74
                                                                                                                                                                  130;
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                                                                                                                                                                    Conservative
                                                                                                                                                                                 35.4%;
45.8%;
                                                                                                                                                                  48;
                                                                                                                                                              Score 594; DB 4;
Pred. No. 1.7e-50;
8; Mismatches 92
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                                                                                                                                                                                                         Length 431;
                                                                                                                                                                  Indels
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                                                                                                                                                              Gaps
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                                                                                                                                                             RESULT 8
US-08-852-743-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-442-5
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                                                                                                                      Sequence 2, Application US/08852743 Patent No. 5830699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 35.4%; Score 594; DB 4; Length 431; Best Local Similarity 45.8%; Pred. No. 1.7e-50; Matches 130; Conservative 48; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 5
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                                        GENERAL INFORMATION:
APPLICANT: Force, Thomas
APPLICANT: Kyriakis, John
APPLICANT: Pombo, Celia N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE FILLE REFERENCE: PHM. 70296. N1
CURRENT APPLICATION NUMBER: US/09/468,442
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/340,993
EARLIER FILING DATE: 1999-06-25
EARLIER FILING DATE: 1999-06-25
EARLIER FILING DATE: 1997-12-19
EARLIER FILING DATE: 1997-12-19
EARLIER FILING DATE: 1998-12-15
EARLIER FILING DATE: 1998-12-15
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APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
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                        APPLICANT:
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                                                                                                                                                                                                                                        EFVEACLNKEPSFRPTAKELLKHKFILRNAKKTSYLTELIDRYK 292
                                                                                                                                                                                                                                                                   NFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPT-VIMDLIQRTK 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKLRHPNTIQYRGCYLREHTAWLYMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 139
                                                                                                                                                                                                                                                                                                                      --KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE-GNYSKPLK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQCDSPYVTKYYGSYLKDTKLWIIMEYLGGGSALDLLE--PGPLDETQIATILREILKGL 132
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                      Bonventre, Joseph
                                        Pombo, Celia M.
                                                           Kyriakis, John M.
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US-09-211-930-4

US/09211930

GENERAL INFORMATION: Sequence 4, Application Patent No. 5962265

APPLICANT: Tyrell E. No. 5962265r: APPLICANT: William Craig Moore APPLICANT: David Shay Silberstein

5962265ris

TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION TITLE OF INVENTION: SERINE/THREONINE KINASE

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Matches 128;
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FILING DATE: 7-MAY-127.

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: 60/016,774

APPLICATION NUMBER: 7-MAY-1996

TITTING DATE: 7-MAY-1996
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,
FILING DATE: 7-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 7-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SOK-1 AND METHODS NUMBER OF SEQUENCES: 10
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247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
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              VDSCLQKIPQDRPTSEVLLKHRFVLR-ERPPTVIMDLIQRTK 298
                                                                                                                                                                                                                                 LRHPNTIQYRGCYLREHTAWLYMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141
VEACLNKDPRFRPTAKELLKHKFITRYTKKTSFLTELIDRYK
                                                                                     DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF 257
                                                                                                                                          LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
                                                                   KQSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKNSPPTLEGQH-SKPFKEF
                                                                                                                                                                           LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 197
                                                                                                                                                                                                           CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY 130
                                                                                                                                                                                                                                                                                    DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL -- EEAEDEIEDIQQEITVLSQ 72
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                                                                                                                                                                                                                                                                                                                                                                        34.3%;
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                                                                                                                                                                                                                                                                                                                                                         ; Score 576; DB 2;
; Pred. No. 9.9e-49;
48; Mismatches 92
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288
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-340-993-4
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LENGTH: 426
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SEQ ID NO 4
LENGTH: 426
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                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE FILE REFERENCE: PHM.70296.N1
CURRENT APPLICATION NUMBER: US/09/340,993
CURRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tyrell E. No. 6034228ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
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CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT FILING DATE: 1998-12-15
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: GB 9726851.0 & US EARLIER FILING DATE: 1997-12-19 & 1998-12-15 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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                                                                                                                                                         23 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                            Local Similarity
LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 197
                                                                                                                   DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEACLNKDPRFRPTAKELLKHKFITRYTKKTSFLTELIDRYK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDSCLQKIPQDRPTSEVLLKHRFVLR-ERPPTVIMDLIQRTK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEGGYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 197
                                        CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY 130
                                                                            LRHPNTIQYRGCYLREHTAWLYMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL -- EEAEDEIEDIQQEITVLSQ 72
                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                            34.3%; Score 576; DB 3; 45.4%; Pred. No. 9.9e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.3%; Score 576; DB 2; 45.4%; Pred. No. 9.9e-49;
                                                                                                                                                                                                      48;
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US-09-185-370-2
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US-09-185-370-2
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                                                                                                                                                           Query Match
Best Local Similarity 45.4
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                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bonventre, Joseph TITLE OF INVENTION: SOK-1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
142 LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM
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CITY: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson, STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02110-2804
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                                                                                                          DPEELFTKIJRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ 72
                                                                                                                                       DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                             LRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141
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                                                                                                                                                                                                                                                                                                               426 amino acids
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                                                                                                                                                                      34.3%; Score 576; DB 3;
45.4%; Pred. No. 9.9e-49;
tive 48; Mismatches 92;
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131 LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---

187

EARLIER FILING DATE:

EARLIER APPLICATION NUMBER: GB 9726851.0

1997-12-19

Length 426; Indels

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RESULT 13
US-09-468-442-4
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                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09468442 Patent No. 6300098
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REFERENCE: PHM. 70296.N1
CURRENT APPLICATION NUMBER: US/09/468.442
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/340,993
EARLIER FILING DATE: 1999-06-25
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EARLIER APPLICATION NUMBER: 9719920.2
EARLIER FILING DATE: 1997-09-19
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APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN STE20-LIKE STRESS ACTIVATED
TITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70272
CURRENT APPLICATION NUMBER: US/09/152,406
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ORGANISM: Homo Sapiens
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US-08-712-709-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08712709 Patent No. 5863780
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LENGTH: 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version
                                                                                                                INFORMATION FOR SEQ ID NO:
                                             SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
                                                                                                                                                                                                                                              FILING DATE: Filed Herew.
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                   TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Guegler, Karl J. APPLICANT: Hawkins, Phillip R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
STATE: CA
                                                                                                                                                   TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI--- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 141 | : | : | : | : | 1
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                                                                                                                                                       415-845-4166
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Pred. No. 9.9e-49;
8; Mismatches 92;
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RESULT 15
US-09-111-444-8
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Best Local Similarity 39.7
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
                           ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO:
                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                STREET: 31,
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LIBRARY: Gent
-- ONE: 1117791
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                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                     COMPUTER: IBM CON
OPERATING SYSTEM:
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                TELEFAX:
                                                                                                                                       FILING DATE:
                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              ZIP: 94304
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDAVRELDNLOYRKM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QNESPALQSGH-WSEYFRNEVDSCLQKIPQDRPTSEVLLKHREVLRERPPTVIMDLIQRT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRNPPRRQLKKLDEDSLTKQPEEVFDVLEKLGEGSYGSVYKAIHKETGQIVAIKQVPV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANSFYGTPYWMAPEVILAMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKP 122
                                                                                                                                                                                                                                                                                                                                                              CA
                                                                                                                                                                                                                                                                                                                                                                                                  E: Incyte Pharmaceuticals, 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                              U.S.
                415-845-4166
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39.7%; Pred. No. 5.9e-48;
tive 53; Mismatches 117;
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                                                                                                                                                       08/712,709
                                                                  PF-0118
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Search completed: November 22, Job time: 9.29 secs

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                                                                                                                                                                                                                                                                                                                                                                                            Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1117791
9-111-444-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
                                                              238
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                            6
                                                                                                                          RITVIGTPFWMAPEVI---QEIGYNCVADIWSLGITAIEMAEGKRPYADIHPMRAIFMIP
                                                                                                                                              ANSFYGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIA 238
                                                                                                                                                                                                           LQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAP 178
                                                                                          QNESPALQSGH-WSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRT
                                                                                                                                                                                                                                                                                          KQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKP 122
                                                                                                                                                                                                                                                                                                                          LRNPPRRQLKKLDEDSLTKQPEEVFDVLEKLGEGSYGSVYKAIHKETGQIVAIKQVPV-- 63
MDVKLKRQESQQREM
                            KDAVRELDNLQYRKM 312
                                                              TNPPPTFRKPELWSDNFTDFVKQCLVKSPEQRATATQLLQHPFVRSAKGVSILRDLINEA
                                                                                                                                                                                          LTEDETATILQSTLKGLEYLHFMRKIHRDIKAGNILLNTEGHAKLADFGVAGQLTDTMAK
                                                                                                                                                                                                                                                         ---ESDLQEIIKEISIMQQCDSPHVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKT 120
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                          33.9%;
39.7%;
                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 569; DB 3; Pred. No. 5.9e-48;
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           117;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 487;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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1 MPAGGRAGSLKNPNVAFTFFF
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version
Copyright (c) 1993 - 2002
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AAY49897
AAB41663
AAE04366
AAW97677
AAY49896
AAY55942
AB97326
AAY55938
AAY55938
AAB43191
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Compugen Ltd.
                                                                                                           Rat TAO2 kinase.
Human ORFX ORF1427
Human kinase (PKIN
Human KDS2 protein
Novel human protei
Murine SULU3 prote
Human ORFX ORF2955
Human KDS1 serine/
                                                                                                                                                                                                   Description
                                                                       Rat TAO1 kinase.
Human/Murine SULU3
                                                                                                                                                                                                                                                                                                                                  to have
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                                                                                                         protein
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acid	6822	22		33.7	565
S	Ν	22	1269	33.7	565
Nematode STE20-rel	AAY55951	20	443	33.7	565
Human h2252 protei	AAB66607	22	416	ω	567
Human TGF-beta rec	AAB71958	22	416	ω	567
Human polypeptide	AAM40348	22	416	w ·	567
	AAY82277	21	416	ω.	567
Human Ste20-like s	AAY82274	21	416	ω	567
Murine 5e.new poly	AAY21673	20	416	ω	567
A murine signal tr	AAY22651	20	416	ω.	567
D)	AAY22648	20	416	ω.	567
Human STLK2 protei	AAY55927	20	416	ω.	567
Human polypeptide,	AAM93576	22	392	ω.	567
Human Ste20 homolo	AAY21674	20	487		574
Drosophila melanog	ABB65561	22	596	4.	574.5
Human MAPK-pathway	AAY82275	21	426	4.	576
Human STE20 protei	AAY55949	20	426		576
	AAW31603	18	426	4.	576
Novel human diagno	ABG04990	22	458	4.	581
acid sequ	AAY68771	21	431	5	588
Ø	AAY21672	20	413	35.2	591
n-N-kinas	AA020953	23	443	35.4	594
Human Ste20-like k	AAY82276	21	431	35.4	594
Human STE20-like s	AAY04473	20	431	5	594
Human MST3 protein	AAY55950	20	431	5	594
Human polypeptide	AAB97069	22	431	35.5	596
protein	AAM25383	22	163	9.	660
otein seq	AAB95890	22	398	۳.	703
$\sim$	AAY55955	20	982	0.	1008
4	AAU17256	22	265	5	1092
Novel central nerv	AAU87435	22	265	65.1	1092
1 centr	8711	22	323	69.0	1158
phila melano	6911	22	1039	ω	9
SULU1 prote	Y559	20	898	82.4	ω
Human cell signall	AAY44244	21	898	82.5	1384

## ALIGNMENTS

RESULT 1
AAY49897
ID AAY4

AAY49897 standard; Protein; 993

A

AAY49897;

Rat TAO2 kinase.

27-JAN-2000 (first entry)

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TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder;
                    WPI; 1999-633831/54.
N-PSDB; AAZ32436.
                                                Cobb M,
New polypeptides that phosphorylate kinase,
                                                                                      14-APR-1998;
                                                                                                        14-APR-1999;
                                                                                                                            21-OCT-1999
                                                                                                                                               W09953076-A1
                                                                                                                                                                 Rattus sp
                                                                   (TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                                                    neurodegeneration; MAP kinase; MAP/ERK kinase
                                                Hutchison M,
                                                                                      98US-0060410
                                                                                                        99WO-US08165
                                               Chen Z,
                                                Berman
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 used to screen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents rat TAO2 protein kinase, which is capable of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related polypeptides, are used to screen for modulators of stress-responsive mitogen activated protein (MAP) kinase pathways. These modulators are potentially useful for treating or preventing: (1) inflammation, autoimmune disease, cancer and degeneration (inhibitors of phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders and neurodegeneration (enhancers of phosphorylation). TAO kinases are modulators and as immunoassay reagents for detecting TAO kinases. TAO kinases polynucleotides can be used: (a) for recombinant expression of TAO kinases; and (b) in the form of fragments, for detecting TAO kinase polynucleotides in standard hybridisation and amplification tests. TAO kinases are highly specific for MEK3.
allergy; apiastic anacm
bone damage; cartilage
                                          hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antifuematic; antithyroid; antithanaemic; gene therapy; cancer; proliferative disorder; hypottension neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
                                                                                                                                                                              Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                                                                                                                                                 Human ORFX ORF1427 polypeptide sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                    AAB41663 standard; Protein; 1235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modulators for treating e.g. cancer or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRELDNLQYRKMKKILFQEA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFYGTPYWMAPEVILAMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320;
                          aplastic anaemia; nocturnal haemoglobinuria; burn; wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 84-87; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      993 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; llarity 100.0%; Conservative C
                                                                                                                                                                                                                                                                                                                         (first entry)
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Pred. No. 1
      antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                         hypertension;
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                                                                                                                                                                                                                                                                                                                                                                                   which represent the human ORFX open reading frames 1 to 3161. The ORFX CS sequences have activities such as: cytostatic, hepatotropic; vulnerary; CC antipacoriatic; antiparkinsonian; noctropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; cantidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; can hithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating the presence of or predisposition to, or preventing or treating compatibilities as a second with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy certors. The proteins and nucleic acids may be used to treat cancers, cordiferative disorders, neurodegenerative disorders, osteoarthritis, corpoliferative disease, cardiovascular disease, diabetes mellitus, typertension, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, allerdise, aplastic anaemia, hurns, wounds hone and cartilage damage.
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                            allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 2092-2095; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
N-PSDB; AAC75872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC74446 to AAC77606 encode the proteins given in AAB40237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                 Local
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 ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA
                                MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
                                                                                                                                     KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN
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                                                                                                                                                                                                                                                                                                                 319;
                                                                                                                                                                                                                                                                                                                                 Similarity
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99US-0127728.
2000US-0540763.
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99.7%;
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Pred. No. 4.5e-162;
                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                            Length 1235;
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RESULT 3
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          The invention relates to novel human kinase proteins (PKIN) and nucleic acid molecules encoding them. PKIN is useful for identifying compounds that modulates its activity. PKIN cDNA is useful for assessing toxicity of a test compound. PKIN and its cDNA are useful for diagnosis, prevention and treatment of immune disorders such as acquired immune deficiency syndrome (AIDS), Addison's disease, anaem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human kinase; PKIN-7; therapy; immune disorder; Addison's disease; AIDS; acquired immune deficiency syndrome; growth and developmental disorder; arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma; leukaemia; cardiovascular disease; myocardial infarction; hypertension; lipid disorder; cancer; fatty liver; cholestasis; transgenic animal; gene therapy; antiallergic; antialsthmatic; antithyroid; dermatological; antidiabetic; nephrotophic; antiulcer; antiarthritic; antitrheumatic; antipsoriatic; neuroprotective; cytostatic; hepatotrophic; osteopathic;
                                                                                                                       Novel human kinase proteins (PKIN) useful for diagnosing, treating, preventing immune disorders, cardiovascular diseases and disorders affecting growth and development associated with abnormal expression
                                                                                                                                                                                                                                                              23-DEC-1999; 99US-0172066.
14-JAN-2000; 2000US-0176107.
21-JAN-2000; 2000US-0177731.
28-JAN-2000; 2000US-0178573.
                                                                                          Claim
                                                                                                                                                                                                        Yang J,
Yao MG,
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                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                    Yang
                                                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                                      20-DEC-2000; 2000WO-US35304
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  respiratory
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                                                                                                                                                                                                      Baughn
Lal P,
                                                                                         Page 111-113; 128pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antianginal; anorectic
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618..777
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147..158
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distress syndrome,
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                                                                                                                                                                                                        FA;
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WPI; 1999-120900/10
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis and diabetes mellitus; growth and developmental disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD),
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                                                                                                                                       (CADU-)
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                                                                                                                                                                                                             97US-0889518
                                                                                                                                                                                                                                                                                      98WO-US14231
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Best Local
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               TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder;
                                                                                                                               Rat
                                                                                                                                                                               27-JAN-2000
                                                                                                                                                                                                                                                                                    AAY49896 standard; Protein; 1001 AA
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neurodegeneration; MAP kinase; MAP/ERK kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
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                                                                                                                               TAO1 kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription. KDS polypeptides and polynucleotides can be for treating disorders involving aberrant expression of alian KDS genes. They can also be used for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                    VRELDNLQYRKMKKILFQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                               VRELDNLQYRKMKKILFQEA 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and drug screening.
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97.8%;
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Pred. No. 8.4e-159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders and neurodegeneration (enhancers of phosphorylation). TAO kinases are also used to raise specific antibodies, useful therapeutically as modulators and as immunoassay reagents for detecting TAO kinases. TAO kinase polynucleotides can be used: (a) for recombinant expression of TAO kinases; and (b) in the form of fragments, for detecting TAO kinase polynucleotides in standard hybridisation and amplification tests. TAO kinases are highly specific for MEX3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents rat TAO1 protein kinase, which is capable of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related polypeptides, are used to screen for modulators of stress-responsive mitogen activated protein (MAP) kinase pathways. These modulators are potentially useful for treating or preventing: (1) inflammation, autoimmune disease, cancer and degeneration (inhibitors of
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides that phosphorylate kinase, used to modulators for treating e.g. cancer or inflammation % \left( 1\right) =\left\{ 1\right\} 
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                                                                             ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA 300
                                                                                                                                                                                      KPLQEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN
                                                                                                                                                                                                      KPLQEVEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN 180
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                                                                                                                          SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
                                                                                                                                                       SFYGTPYWMAPEVILAMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
                                                                                                                                                                                                                                                   YSGKQSTEKWQDIIKEVKFLQRIKHPNSIEYKGCYLREHTAWLVMEYCLGSASDLLEVHK 120
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VRELDNLQYRKMKKLLFQEA
                                                             ESPTLQSNEWSDYFRNFVDSCLQKIPQDRPTSEELLKHMFVLRERPETVLIDLIQRTKDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1001 AA;
                                                                                                                                                                                                                                                                                                                                                                            Conservative
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88.8%;
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                                                                                                                                                                                                                                                                                                                                                                          Score 1529; DB 20;
Pred. No. 2.4e-147;
2; Mismatches 14;
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RESULT 6 AAY55942

AAY55942

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Peptide;

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                                                                                                                                                                                                                                                                                                                                                    CC This sequence represents a consensus peptide sequence conained in novel CC STE20-related protein kinases. The invention relates to a nucleic acid conclude encoding a kinase polypeptide selected from STLK2, STLK3, STLK4, CC STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 CC and PAK5. The proteins are used to identify agonists and antagonists, and Ct to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, polypeptides, antibodies, antagonists and cc agonists may be used to treat diseases such as immune-related disorders cand diseases (e.g. rheumatoid arthritis, artherosclerosis, chronic costeoarthritis, psoriasis, atherosclerosis, arthaction, asthma, costeoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, candory of transplantation, chronic inflammatory pelvic disease, multiple collegosis, organ transplantation, myocardial infarction, cardiovascular collegoses, stroke, renal failure, oxidative stress related concurders disease and Leigh syndrome), cancer, cardiomyopathies, atherosclerosis, cancer, cardiomyopathies, cancer, cardiomyopathie
                                                                                                        Matches
                                                                                                                                                        Query Match
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                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel kinase-related polypeptides used for the diagnosis and treatment of kinase-related diseases and disorders \,
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                                                                                                                                                                                                                                                                         ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growtl regulation (e.g. in wound healing), T cell activation, mitosis control,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11;
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                                                                                                                                                                                                              1001 AA;
                                                                                                        Conservative
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RESULT 7
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                                            (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT,
Xue AJ,
                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of novel human proteins. These were isolated from expressed sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                An isolated polynucleotide for treating diseases associated with its encoded polypeptide such as cancer and multiple sclerosis - \!\!\!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-292408/33.
N-PSDB; ABN32512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene t neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB97326 standard;
                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 594; 509pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Asundi V, Zhang
T, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ren
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Similarity

91.0%; Score 1527; DB 23; 88.8%; Pred. No. 3.9e-147;

Length

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RESULT 8
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                                                                                                                                                                                                                                                                                                                 neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic; vulnery, STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7; 2C1; 2C2; 2C3; 2C4; KHS2; SULU1; SULU3; GEKZ; PRA4; PAK5; antagonist; antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma; inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis; rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure; oxidative stress-related neurodegenerative disorder; parkinson's disease; amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; ischemic disorder; growth regulation; wound healing; T cell activation; mesangial disorder; growth regulation; wound healing; T cell activation;
Novel kinase-related polypeptides used for the finase-related diseases and disorders
                                             N-PSDB;
                                                                                                                                                      14-APR-1998;
                                                                                                                                                                                                                                               WO9953036-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
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                                            1999-611301/52.
DB; AAZ40490.
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                                                                                                                        SUGEN
                                                                                          Martinez
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               and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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          Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiparkintic; immunosuppressant; cardiant immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antiencerial; antimpal; antirheumatic; antithyroid; antiviral; antienceri; proliferative disorder; hypertension neurodegenerative disorder; osteoarthritis; graft w host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                         Human ORFX ORF2955 polypeptide sequence
                                                                                                                                                                                                                                 08-FEB-2001
                                                                                                                                                                                                                                                                                                          AAB43191 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                          VRELDNLQYRKMKKLLFQEA
                                                                                                                                                                                                                                                                                                                                                                                                                                               VRELDNLQYRKMKKILFQEA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFYGTPYWMAPEVILAMDEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPLQEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSGKQSTEKWQDIIKEVKFLQRIKHPNSIEYKGCYLREHTAWLVMEYCLGSASDLLEVHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESPTLQS---
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277; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Page 299-301; 387pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        748
                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----NMNDSCLQKIPQDRPTSEELLKHMFVLRERPETVLIDLIQRTKDA
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diabetes
                                                                                                                                                                                                                                                                                                                                                                                                             312
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Pred. No. 3.6e-141;
11; Mismatches 14;
                                                                                                                                                                                           SEQ ID
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                                                                                                                                                                                             NO:5910
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LK7, ZC1, ZC2, ZC3,
                                      hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                                                                cardiant;
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Best Local :
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                            allergies, aplastic anaemia, burns, wounds, bone and cartilage (nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic namemia; nocturnal haemoglobhnuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CURA-) CURAGEN CORP.
                                        122
186 PYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPAL
                                                                          126
                                                                                                             62
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                                                                                                          RAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQ
                                   VEIAAITHGALHGLAYLHSHALIHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVGT
                                                      VEIAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEDGLVKLGDEGSASIMAPANSFYGT 185
                                                                                                                                           SNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQE 125
                                                                                                                                                                               RKGVLKDPETADLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTSEVVAIKKMSYSGKQ
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 5088-5090; 5507pp; English.
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99US-0127636.
99US-0127728.
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                                                                                                                                                                                                                                                                        Score 1392;
Pred. No. 2
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2.3e-133;
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                                                                                                                                                                              This polypeptide comprises human serine/threonine kinase KDS1, a novel protein associated with signal transduction. KDS1 has a K kinase domain related to that of Ste20 (KDS1 = Kinase Domain C related to Ste20). KDS1 cDNA (see AAX07074) was isolated from a C human bone marrow cDNA library. A clone (see AAX07075) encoding the highly homologous KDS2 (see AAW97677) was also obtained. Both KDS1 and KDS2 have Glu/Gln-rich regions at their C-terminus (see also AAW97678-79) suggesting an alpha-helical structure that may play a role in covalently localising these proteins to a specific site within the cells, which may be necessary for function. A method for producing KDS polypeptides in host cells is provided. Since KDS molecules have kinase activity, they are useful as modulating a gents in regulating a variety of cellular processes such as signal transduction pathways. These pathways may regulate cytoskeleton,
                                                                                                                    secretion, growth, apoptosis, superoxide generation, and spengene transcription. KDS polypeptides and polypucleotides caused for treating disorders involving aberrant expression of mammalian KDS genes. They can also be used for detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated vertebrate kinase - used to develop products for the diagnosis and treatment of disorders involving cellular processes
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                                                                      Sequence
                                                                                                      diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           threonine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDS1; kinase domain related to Ste20; human; serine kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human KDS1 serine/threonine kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 PYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSPTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signal transduction processes
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 78-81; 100pp; English.
                                                                      868
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                                                                                                    genes. They ca
drug screening.
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Score 1389; DB Pred. No. 4.6e-12; Mismatches
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Matches

Conservative

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Query Match
Best Local Similarity

82.8%; 81.5%;

Length Indels

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Gaps

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RESULT 11
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IDY 4244
XX AAY4
AXC AAY4
XX AAY4
AXC AAY4
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KW Infl
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FT Mod:
FT Mod:
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4
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Bandman O,
Baughn MR,
                                    The present sequence is cell signalling protein-7 (CSIGP-7) encoded by cDNA obtained from Incyte clone 2948818 of KIDNFET01 library. It is expressed in reproductive, haematopoietic/immune and nervous tissues and is found to be homologous to serine/threonine protein kinase. Fragments of CSIGP encoding nucleic acid can be used as hybridisation probe for detecting CSIGP related sequences or allelic variants. Recombinant CSIGP can be produced in host cells by transforming them with genetically engineered vectors. Agonists or antagonists can be used in the treatment of cell proliferative and inflammatory disorders associated with decreased or increased CSIGP expression. CSIGP is used in
                  the diagnosis, prevention and treatment of cell proliferative disorders like arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
                                                                                                                                                         Claim 1;
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                                  N-PSDB; AAZ40488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure; oxidative stress related neurodegenerative disorder; Parkinson's disease; oxidative stress related neurodegenerative disorder;
                                                                 WPI; 1999-611301/52
                                                                                                                      Plowman G,
                                                                                                                                                                                                                                            14-APR-1998;
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ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.5%;
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Pred. No. 1.5e-132;
31; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wound healing;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a novel STE20-related protein kinase. The Invention relates to nucleic acid molecule encoding a kinase polypeptide selected from STEX2, STEAM, ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pelvic disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amylotrophic lateral sclerosis, parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.
                                                                         Drosophila melanogaster
                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 34140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel kinase-related polypeptides used for the diagnosis of kinase-related diseases and disorders \, -
                                                                                                                                                                                                                                                          26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     ABB69116 standard; Protein; 1039 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLQYRKMKKILFQE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLQYRKMKKILFQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEIAAITHGALHGLAYLHSHALIHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKGVLKDPEIDDLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTNEVVAIKKMSYSGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 898
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81.2%;
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Pred. No. 1.9e-132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The inventi useful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

[ABB57737-ABB72072).
            Novel central nervous
                                                                    AAU87114 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656860/75.
N-PSDB; ABL13219.
                              05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 34140; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genes
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                      specification,
                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
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                                                                                                                                                                                             VRELDNLNYRKMKKIL
                                                                                                                             VRELDNLQYRKMKKIL
                                                                                                                                                                                                                                              KPLQEVETAAVTHGALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPAN 180
                                                                                                                                                                                                                                                                                  YSGKQSNEKWQDIIKEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHK 120
                                                                                                                                                         ESPTLPKNDWSDAFCSFVELCLKKMPAERPSSAKLLTHAYVTRPRSDTVLLELIARTKSA
                                                                                                                                                                   ESPALQSGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRERPPTVIMDLIQRTKDA
                                                                                                                                                                                                                                                                                                               MPS-ARPGSLKDPEIADLFNKHDPEKIFEDLREIGHGSFGAVYYARCNLTREIVAIKKMS
                                                                                                                                                                                                                                                                                                                                 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMS
                                                                                                                                                                                                                                                                                                                                                    233;
                                                                                                                                                                                                                                    KPLHEDEIAAICLGVLSGLSYLHSLGRIHRDIKAGNILLTDNGVVKLADFGSAAIKCPAN
                                                                                                                                                                                                                                                                         YTGKQSQEKWQDILKEIRFLRQLNHPNTIEYKGCYLRESTAWLVMEYCVGSASDIIEVHK
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                                                                                                                                                                                                                                                                                                                                                                                                                    but was obtained in electronic format directly from WIPO
                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                             73.9%;
73.7%;
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           system
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                                                                     323
                                                                                                                                                                                                                                                                                                                                                            Score 1239.5; DB 2
Pred. No. 1.2e-117;
           protein #24
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  14-AUG-2000;

14-AUG-2000;

18-AUG-2000;

22-AUG-2000;

22-AUG-2000;

23-AUG-2000;

23-AUG-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

01-SEP-2000;

05-SEP-2000;

06-SEP-2000;

06-SEP-2000;

08-SEP-2000;

14-SEP-2000;

14-SEP-2000;
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07-JUL-2000;
07-JUL-2000;
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16-MAR-2000;
17-MAR-2000;
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14-AUG-2000;
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26-JUL-2000;
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19-MAY-2000
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2000US-0214886
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acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; anglogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; food preservative; gene therapy.

2001WO-US01332.

2000US-0198123 2000US-0205515 2000US-0189874 2000US-0186350 2000US-0184664 2000US-0180628 2000US-0179065

2000US-0215135. 2000US-0216647. 2000US-0216880. 2000US-0217487. 2000US-0217496. 2000US-0218290 2000US-0220963

2000US-0220964. 2000US-0224518. 2000US-0224519. 2000US-0225213. 2000US-0225214.

2000US-0225266. 2000US-0225267. 2000US-0225268. 2000US-0225270. 2000US-0225447. 2000US-0225757. 2000US-0225759. 2000US-0225759. 2000US-0225759.

2000US-0226681. 2000US-0228868. 2000US-0227182. 2000US-0227109. 2000US-0228924. 2000US-0229343. 2000US-0229343. 2000US-0229344.

2000US-0229509. 2000US-0229513. 2000US-0230437.

2000US-0230438. 2000US-0231242. 2000US-0231243.

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08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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25-SEP-2000

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26-SEP-2000

27-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

29-SEP-2000

20-OCT-2000

02-OCT-2000

02-OCT-2000

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02-OCT-2000

03-OCT-2000

03-OCT-2000

04-NOV-2000

08-NOV-2000

08-NO
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2000US-0249213.
2000US-0249215.
2000US-0249215.
2000US-0249216.
2000US-0249217.
2000US-0250391.
2000US-0251030.
2000US-0251988.
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2000US-0249209.
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Matches
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                                                                                              disorders e.g. testicular feminisation, endocrine disorders e.g. diabet and pituitary dwarfism, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The
                                                                                                                                                                                                                                                  disorders e.g. neoplasms of the breast or liver, cardiovascular disorder e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. dysphagia, dedenocarcinomas and irritable bowel syndrome, reproductive system
                                                                                                                                                                                                                                                                                                                                                                                                       novel ce
by (I),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen
                                                                                   primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to
                                                                                                                                                                                                                                                                                                                                                                      autoimmune diseases e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABK43444.
                                                                                                                                                                                                                                                                                                                                                                                     pathological condition. Disorders which are diagnosed or treated include
 Local Similarity 88.1
les 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     invention describes an isolated nucleic acid molecule (I) encoding a el central nervous system protein. (I) and polypeptides (III) encoded (I), are used to treat a medical conditions and in diagnosis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           additives or preservatives
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2000US-0251990.
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2000US-0259678.
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                                                                  storage capabilities, fat content, lipid,
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                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis, hyperproliferative
15;
Score 1158; DB 2
Pred. No. 5e-110;
5; Mismatches 1
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                               DB 22;
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                                                  DSCLQKIPQDRPTSEELLKHIFVLRERPETVLIDLIQRTKXAVRELDNLQYRKMXKLLFQ
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2000US-0199076.
2000US-0199076.
2000US-0199467.
2000US-0216647.
2000US-0216647.
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2000US-0218290.
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neoplasm; cardiovascular disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amylotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosts of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; SEQ ID No 953; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used food additives or preservatives -
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                       LGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNFVDSCLQKIPQDRP 270
                                                                                                  DVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVILAMDEGQYDGKVDVWS 210
LGITCIELAERKPPLFNMNAMSALYHIAQNESPTLQSNEWSDYFRNFVDSCLQKIPQDRP
                                                                            DIKAGNILLTEPGQVKLADFGSASMASPANSFVGTPYMMAPEVILAMDEGQYDGKVDVWS 120
                                                                                                                                                       YKGCXLREHTXWLVMEYCLGSASDLLEVHKKPLQEVETAAITHGALQGLAYLHSHTMIHR 60
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2000US-0251988.
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                                                                                                                                                                                                                                65.1%; Score 1092; 189.5%; Pred. No. 2.20 Live 11; Mismatches
                                                                                                                                                                                                                                DB 22;
2.2e-103;
nes 13;
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diabetes

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271 TSEVLLKHRFVLRERPPTVIMDLIQRTKDAVRELDNLQYRKMKKILFQ 318

180

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Gaps

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181 TSEELLKHIFXLRERPETVLIDLIQRTKDAVRELDNLQYRKMKKLLFR
 228
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Search completed: November 22, Job time: 24.52 secs 2002, 12:23:37

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Result
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Maximum DB
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Perfect score:
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                         Human/Murine SULU3
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Human ORFX ORF2955
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                                                                                                                                                                                                                                                                          Rat TAO2 kinase.
Human ORFX ORF1427
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Amino acid sequenc	AAB68223	22	1269	37.6	537.5
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=	ABB65561	22	9	8	555
h2252 pro	AAB66607	22	$\vdash$	39.0	57
	AAB71958	22	$\vdash$	9	57
polypept	AAM40348	22	₩.	9	57
Mouse protein segu	AAY82277	21	μ.	9	57
Ę.	AAY82274	21	$\vdash$	9	57
e.new	AAY21673	20	$\vdash$	9	57
e signal	AAY22651	20	$\mathbf{\mu}$	9	57
nal tr	AAY22648	20	$\vdash$	9	57
STLK2 prote	AAY55927	20	$\vdash$	9	57
Human polypeptide,	AAM93576	22	9	9	57
MAPK-pathwa	AAY82275	21	2	9.	83
STE20 pr	AAY55949	20	Ν	9	89
5	AAW31603	18	Ν	9	89
human	ABG04990	22	458	40.0	571.5
Amino acid sequenc	AAY68771	21	ω	0	78
e C12.2bs	AAY21672	20	$\vdash$	0	81
-N-kina	AAO20953	23	4	0	84
Ste20-like	AAY82276	21	ω	0	84
STE20-like	AAY04473	20	431	0	84
Human MST3 protein	AAY55950	20	w	0.	84
polypept	AAB97069	22	ω	1	98
n seq	AAM25383	22	σ	6.	660
Nematode STE20-rel	AAY55955	20	982	÷	883
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phila m	69	22	ω	6.	0
SULU1 F	5593	20	898	4	1202
Human cell signal	AAY44244	21	9	4	

## ALIGNMENTS

RESULT 1 AAY49897

AAY49897 standard; Protein; 993 AA.

Rat TAO2 kinase. 27-JAN-2000 AAY49897;

(first entry)

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TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder; neurodegeneration; MAP kinase; MAP/ERK kinase.
                   WPI; 1999-633831/54.
N-PSDB; AAZ32436.
New polypeptides that phosphorylate kinase, used to screen for
                                                Cobb M,
                                                                                                                               21-OCT-1999.
                                                                                                                                                                    Rattus sp.
                                                                                        14-APR-1998;
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                                                                                                                                                 WO9953076-A1
                                                                    (TEXA ) UNIV TEXAS SYSTEM.
                                                Hutchison M,
                                                                                        98US-0060410
                                                                                                           99WO-US08165
                                                Chen
                                                z,
                                                Berman
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W Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; KW hypotensive; dermatological; immunosuppressive; antithflammatory; KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid; KW antianaemic; gene therapy; cancer; proliferative disorder; hyportension; KW neurodegenerative disorder; osteoarthritis; graft vs host disease; KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; KW cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; KW brome damage; cartilage damage; antiinflammatorv disease.
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                                                                                                                                                                                                                                                                                                                                     Human ORFX ORF1427 polypeptide sequence SEQ ID NO:2854.
                                                                                                                                                                                                                                                                                                                                                                                08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB41663 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, CC which represent the human ORFX open reading frames 1 to 3161. The ORFX CS sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; cosquilant; vasotropic; CC antidiabetic; hypotensive; dermatological; immunosuppressive; antirheumatic; antiarthritia; antiviral; antifungal; antirheumatic; CC antithyroid; and antianaemic. The sequences can be used for determining CC the presence of or predisposition to, or preventing or treating CC pathological conditions associated with an ORFX-associated disorder. The CC nucleic acids can be used to express ORFX proteins in gene therapy CC vectors. The proteins and nucleic acids may be used to treat cancers, CC proliferative disorders, neurodegenerative disorders, osteoarthritis, CC graft vs host disease, cardiovascular disease, diabetes mellitus, CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, CD bacterial or fungal infection, malaria, autoimune disorders, asthma, CC corguilation. To inhihit thrombosis. and as a contracerive
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coagulation; to inhibit thrombosis; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 2092-2095; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
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                                                                                                                                                     ALQGLAYLHSHUMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWWAPEVI 180
RNFVDSCLQKIPQDRPTSEVLLKHRFVLRER 271
                                                                         LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF
                                                                                                                                                                                                                                                KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG
                                                                                                                                 ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVI
                                                                                                                                                                                                            KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG
                                                                                                                                                                                                                                                                                      VAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDII 74
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                                                       LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPVLQSGHWSEYF
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               1235
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99US-0127636.
99US-0127728.
99US-0540763.
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 99.7%;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 1424; DB 21; Pred. No. 6.8e-142;
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                     Length 1235;
                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 3
AAE04366
14-JAN-2000;
21-JAN-2000;
28-JAN-2000;
        for diagnosis, prevention and treatment of immune disorders such as acquired immune deficiency syndrome (AIDS). Addison's disease, anaemia, adult respiratory distress syndrome, allergies, amyloidosis, psoriasis, autoimmune haemolytic anaemia, autoimmune thyroiditis, multiple sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis, ulcerative colitis and diabetes mellitus; growth and developmental disorders such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), and myelofibrosis; cancers such as adenocarcinoma and leukaemia, cardiovascular diseases such as myocardial infarction and hypertension; and input diseases such as myocardial infarction and hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human kinase; PKIN-7; therapy; immune disorder; Addison's disease; AIDS; acquired immune deficiency syndrome; growth and developmental disorder; arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma; leukaemia; cardiovascular disease; myocardial infarction; hypertension; lipid disorder; cancer; fatty liver; cholestasis; transgenic animal; gene therapy; antialiergic; antiasthmatic; antithyroid; dermatological; antidiabetic; nephrotophic; antiulcer; antiarthritic; antirheumatic; antipsoriatic; neuroprotective; cytostatic; hepatotrophic; osteopathic; vasotropic; antianginal; anorectic.
                                                                                                                                                                                                                                                                                              Novel human kinase proteins (PKIN) useful for diagnosing, treating, preventing immune disorders, cardiovascular diseases and disorders affecting growth and development associated with abnormal expression
                                                                                                                                                                                                                                                                                                                                                                                                                               Yang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE04366 standard;
                                                                                                                                                                   The invention relates to novel human kinase proteins (PKIN) and nucleic acid molecules encoding them. PKIN is useful for identifying compounds that modulates its activity. PKIN cDNA is useful for assessing toxicity of a test compound. PKIN and its cDNA are useful
                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                Yang J,
Yao MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human kinase (PKIN)-7.
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                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999;
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DB; AADO8640.
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                                                                                                                                                                                                                                                                                                                                                                                                            Baughn MR,
Lal P, Kh
                                                                                                                                                                                                                                                   Page 111-113;
disorders such as fatty liver and cholestasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0176107.
; 2000US-0177731.
; 2000US-0178573.
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30..26
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                                                                                                                                                                                                                                                                                                                                                                                                                Khan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                               Burford
                                                                                                                                                                                                                                                                                                                                                                                                                FA;
                                                                                                                                                                                                                                                128pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Serine/threonine protein kinase TAO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1049
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                                                                                                                                                                                                                                                  English
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
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This polypeptide comprises human protein kinase KDS2, protein associated with signal transduction. KDS2 has kinase domain related to that of Ste20 (KDS1 = Kinase related to Ste20). KDS2 cDNA (see AAX07075) was isolated to Ste20).
                                                                                                                                                                                     New isolated vertebrate kinase - used to develop products for the diagnosis and treatment of disorders involving cellular processes such as signal transduction processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human KDS2 protein kinase
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                                                                                                                                                                                                                                                                                                                                                                             Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                     (CADU-) CADUS PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195
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DB; AAX07075.
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                                                                                                                                                                                                                                                                                                                                                                                GL,
                                                                                                                                Page 85-88; 100pp;
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Pred. No. 1
                                                                                                                                   English
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1.4e-141;
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Kinase Domain
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Best Local Similarity
WPI; 1999-633831/54
                            Cobb
                                                                                                                 14-APR-1999;
                                                                                                                                            21-OCT-1999
                                                                                                                                                                       WO9953076-A1
                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                              neurodegeneration; MAP kinase; MAP/ERK kinase.
                                                                                                                                                                                                                                         TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation; p38; protein kinase; cancer; inflammation; autoimmune disease; degeneration; insulin-resistant diabetes; metabolic disorder;
                                                                                                                                                                                                                                                                                                      Rat TAO1 kinase
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                                                                                                                                                                                                                                                                                                                                                                                       AAY49896 standard; Protein; 1001 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNFVDSCLQKIPQDRPTSEVLLKHRFVLRER 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEVRFLQKVRHPNTIQYRGCYLREQTAWLVMEYCLGSAFDLLEVHKKPLQEVEIAAVTHG
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                                                       UNIV TEXAS SYSTEM
                            Hutchison M,
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97.8%;
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Pred. No. 3.
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ID AAY59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive; neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic; vulnery; STE20; protein kinase; STEX2; STLX4; STLX5; STLX6; STLX7 SC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GEK2; PAK4; PAK5; antagonist; antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma; inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis; rhinitis; autoimmunity; organ transplantation; multiple sclerosis; rhinitis; antipsic cardiovascular disease; stroke; renal failure; myocardial infarction; cardiovascular disease; stroke; renal failure;
                                                       oxidative stress-related neurodegenerative disorder; Parkinson's disease; amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
                                                                                                                                                                                                                                                                                                                                                                                                               Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human/Murine SULU3 consensus protein sequence.
                             mesangial disorder; growth regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY55942 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Pred. No. 1.5e-130;
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                                wound healing;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a consensus peptide sequence conained in novel STE2O-related protein kinases. The invention relates to a nucleic acid molecule encoding a kinase polypeptide selected from STEX, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GEK2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid anthritis, artherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma, and organ transplantation, chronic inflammatory pelvic disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related contains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurodegenerative disorders (e.g. amylotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of kinase-related diseases
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                                                                                                                                                                                                                                                             KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG 120
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                                                                                                                                               LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF 240
                                                                                                                                                                                              ALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVGTPYWMAPEVI
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                                                                                                 RNFVDSCLQKIPQDRPTSEVLLKHRFVLRER
                                                                                                                                LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPTLQSNEWSDYF
                                                                                                                                                                                                                             ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 312-315; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1001 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                  92.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1314; DB 20;
Pred. No. 2.5e-130;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                285
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                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequences of 444 novel human proteins. These were isolated from expressed sequences tags (ESTs). They can be used to stimulate cell growth, to regulate haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions
                                                                                                                                                                                                                                                                                                                                                       infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antianaemic; vulnerary; antiinflammatory; immunomodulator; antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy; neuroprotective; antiparkinsonian; protein therapy; EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-292408/33.
N-PSDB; ABN32512.
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoded polypeptide such as cancer and multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-SEP-2001; 2001WO-US26015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 594; 509pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated polynucleotide for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-SEP-2000; 2000US-0659671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200222660-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB97326 standard; Protein; 1001
                                195
   241
                                                                                          135
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                                                           181
                                                                                                                                                 75
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                                                                                                                                                                                                       ĀJ,
                                                                                                        ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVI 180
                                                                                                                                                               KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG
   RNFVDSCLQKIPQDRPTSEVLLKHRFVLRER 271
                                             LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF
                                                                                                                                                KEVKFLQRIKHPNSIEYKGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAITHG 134
                                                                                       ALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVGTPYWMAPEVI 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang Y,
                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                              1001 AA;
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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Wehrman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                  92.0%;
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                                                                                                                                                                                                                                                                    17;
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I, Drmanac RT;
                              ELAERKPPLFNMNAMSALYHIAQNESPTLQSNEWSDYF
                                                                                                                                                                                                                                                                 Score 1314; D
Pred. No. 2.5e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases associated 
multiple sclerosis -
                                                                                                                                                                                                                                                                                DB 23;
.5e-130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sclerosis
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                              Length 1001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QA,
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RESULT 8
AAY55938
                                                                                                           cc invention relates to nucleic acid molecule encoding a kinase polypeptide cc selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, CC ZC4, KHS2, STLU1, SULU3, GEZ2, PAK4 and PAK5. The proteins are used to CC identify agonists and antagonists, and to raise antibodies. The polynucleotides collected in gene therapy protocols. The polynucleotides, collected disorders and agonists may be used to treat cc diseases such as immune-related disorders and diseases (e.g. rheumatoid cc rohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, chronic inflammatory bowel disease (e.g. crhinitis, autoimmunity, and organ transplantation, myocardial cc infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amylotrophic lateral cc cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes cardiomyopathies, ischemic disorders inflammatory disorders, diabetes
Best Local Similaria Conservative Matches 236; Conservative
                                                                 Query Match
                                                                                                                                             cardiomyopathies, ischemic disorders, inflammatory disorders, diabete mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rhinitis; autoimmunity; organ transplantation; multiple sclerosis; myocardial infarction; cardiovascular disease; stroke; renal failure; oxidative stress-related neurodegenerative disorder; Parkinson's disease; amylotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy; ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis; mesangial disorder; growth regulation; wound healing; T cell activation;
                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a novel STE20-related protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 299-301; 387pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel kinase-related polypeptides used for the diagnosis and treatment of kinase-related diseases and disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective; cardiant; cerebroprotective; cytostatic; antidiabetic; vulner; STE20; protein kinase; STEK2; STEK3; STEK4; STEK5; STEK6; STEK 2C1; ZC2; ZC3; ZC4; KHS2; SULU1; CEK2; PAK4; PAK5; antagonist; antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma; inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis; biditie.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antirheumatic; antiathritic; antiinflammatory; antiallergic; osteopathic; antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosupressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY55938 standard; Protein; 748 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-1999;
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                                              87.8%;
87.1%;
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                           16;
                         Score 1254; DB 20;
Pred. No. 3.9e-124;
6; Mismatches 11;
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                                                                 Length 748;
                           Indels
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RESULT 9
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                                                                                                                                                                                                                                                                                                                       31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; open reading frame; ORFX; detection; cytostatic; hepatotrop vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotec; anticonvulsant; osteopathic; antiarrhritic; immunosuppressant; carvimunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic hypotensive; dermatological; immunosuppressive; antiinflammatory; antibiacterial; antifungal; antifheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypotter neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; Alexandrical disease; diabetes mellitus; hypothyroidism; disease; disease; diabetes mellitus; hypothyroidism; disease; disease; disease; disease; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; ast allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                                neurodegenerative disorders and cardiovascular disease
                                                                                 Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                              Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone damage; cartilage damage; antiinflammatory disease;
thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200058473-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
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                                                                                                                                                           AAC77400.
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99US-0127636.
99US-0127728.
2000US-0540763.
                                                                                                                                                                                                                              Leach
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nootropic; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypertension;
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Claim 11; Page 5088-5090;

5507pp; English

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RESULT 10
AAW97676
ID AAW97
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AC AAW97
DT 10-M
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DT 10-M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; antionvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antihinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergies, aplastic anaemia, burns, wounds, bone and cartilage on nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                      08-JUL-1997;
                                                                                                                                                                                                              KDS1; kinase domain related to
threonine kinase; protein kinas
                                                                                                                                                                                                                                                                                                                                                                       AAW97676 standard; Protein; 898
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   (CADU-) CADUS
                                                                       07-JUL-1998;
                                                                                                         21-JAN-1999
                                                                                                                                            WO9902699-A1
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                 Human KDS1 serine/threonine kinase.
                                                                                                                                                                                                                                                                                                     10-MAY-1999
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Pred. No. 1
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RESULT 1:
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Best Local
            Cell signalling protein-7; CSIGP-7; cell proliferation; arteriosclerosis; inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS; Addison's disease; multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated vertebrate kinase - used to develop products for the diagnosis and treatment of disorders involving cellular processes
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                                                                             signalling protein-7.
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Pred. No. 4e-119;
Prematches 22;
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Matches 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is cell signalling protein-7 (CSIGP-7) encouply cDNA obtained from Incyte clone 2948818 of KIDNFET01 library. expressed in reproductive, haematopoletic/immune and nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bandman
Baughn M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissues and is found to be homologous to serine/threonine protein kinase. Fragments of CSIGP encoding nucleic acid can be used as
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N-PSDB; AAZ29228.
               antipsoriatic;
                              Antirheumatic;
                                                           Human SULU1 protein
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Yang J;
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antiathritic; antiinflammatory; antiallergic; osteopathic;
antiarteriosclerotic; antiasthmatic; immunosupressive;
e; cardiant; cerebroprotective; cytostatic; antidiabetic;
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Pred. No. 1.4e
28; Mismatches
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l.4e-118;
nes 23;
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CC invention relates to nucleic acid molecule encoding a kinase polypeptide conservation relates to nucleic acid molecule encoding a kinase polypeptide conservation relates to nucleic acid molecule encoding a kinase polypeptide conservation and page the polynucleotine are used to conservation and page therapy protocols. The polynucleotides are useful in gene therapy protocols. The polynucleotides, conservation and adjoints may be used to treat conservation as immune-related disorders and diseases (e.g. rheumatoid arthritis, artherosclerosis, chronic inflammatory bowel disease (e.g. crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, chronic inflammatory bowel disease (e.g. crohn's disease, multiple sclerosis, organ transplantation, myocardial confidence of the polynucleotides and conservative disorders (e.g. amylotrophic lateral sclerosis, Parkinson's disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amylotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, diabetes cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes conservations, first-protice and mesancial disorders.
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Best Local S
Matches 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a novel STE20-related protein kinase.
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                                                                                                                                                                                                                                                                                                                                                             LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF 240
                                                                                                                 ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVI 180
                                                                                                                                                                                                                                                              KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG 120
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                                                                        ALHGLAYLHSHALTHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVGTPYWMAPEVI
                                                                                                                                                                                                                    KEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAITHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is, fibrotic and mesangial disorders. The proteins may also be for cell growth regulation (e.g. in wound healing), T cell ion, mitosis control, and as immunosuppressants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 293-296; 387pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.8e
29; Mismatches
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L.8e-118;
les 23;
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RESULT 13
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Matches
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                                                                                                                                                                                                                            The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                     sequences (ABL0184)
(ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
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                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 34140; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC,
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               121
                                                                                                                                                Local Similarity hes 201; Conserv
                                       74
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                                                                                                                      1 VAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDII 60
ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVI
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DB; ABL13219.
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                                                                                           IADLFNKHDPEKIFEDLREIGHGSFGAVYYARCNLTREIVAIKKMSYTGKQSQEKWQDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG
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                                                                                                                                                  Conservative
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2000US-0614150.
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                                                                                                                                                76.1%; Score 1086; DB 22; 74.2%; Pred. No. 4.7e-106; tive 30; Mismatches 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                  detection reagent for detecting for elucidating cell signalling
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                                                                                                                                                                                                                                            format directly from
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                                                                                                                                                                                                                                                                                                                                                                                                                                     cell-cell
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RESULT 14
AAU87114
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31-JAN-2000

04-FEB-2000

24-FEB-2000

16-MAR-2000

11-MAR-2000

11-MAR-2000

19-MAY-2000

28-JUN-2000

28-JUN-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000

14-JUL-2000

14-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel central nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLSGLSYLHSLGRIHRDIKAGNILLTDNGVVKLADFGSAAIKCPANSFVGTPYWMAPEVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nervous system; CNS; autoimmune disease; rheumatoid arthrioliferative disorder; neoplasm; cardiovascular disorder; arrest; cerebrovascular disorder; ischaemia; anglogenesis; system disorder; Alzheimer's disease; AIDS; ocular disorde;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
2000US-017905
2000US-018656
2000US-018656
2000US-0186350
2000US-019974
2000US-019913
2000US-0209467
2000US-021647
2000US-021647
2000US-0217487
2000US-0225661
2000US-0225513
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2000US-02255447
2000US-0225758
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    22-AUG-2000

23-AUG-2000

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01-SEP-2000

01-SEP-2000

06-SEP-2000

08-SEP-2000

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15-SEP-2000

16-SEP-2000

17-SEP-2000

18-NOV-2000

19-SEP-2000

20-OCT-2000

20-OC
2000US -0227182
2000US -022987
2000US -022987
2000US -0229343
2000US -0229344
2000US -0229343
2000US -0229513
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2000US -0231243
2000US -02311243
2000US -02311243
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2000US -0231268
2000US -0231268
2000US -0231268
2000US -02323081
2000US -0233064
2000US -02334239
2000US -02335836
2000US -02346476
2000US -02366476
2000US -0246477
2000US -0246677
2000US -024600S
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17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

17-NOV-2000;

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cc e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, canadiopenesis, nervous system disorders e.g. Alzheimer's disease and cc amylotrophic lateral sclerosis, infections caused by bacteria, viruses ce.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders ce.g. corneal infection, gastrointestinal disorders e.g. dysphagia, c adenocarcinomas and irritable bowel syndrome, reproductive system cc disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes cc and pituitary dwarfism, cancers and disorders at the cellular level e.g. cleukaemia, disorders e.g. nonallergic rhinitis, renal disorders e.g. cc respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. cc acute kidney failure and blood related disorders e.g. myocardial cell farction. The polypeptides can also be used to aid wound healing and cepithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The company of the content of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 9; SEQ ID No 632; 837pp; English.
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Mismatches

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14-JUL-2000;
26-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                 acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; respiratory disorder; renal disorder; kidney failure; blood disorder; myocardial infarction; wound healing; cell proliferation; skin aging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder
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2000US-0224518.

2000US-0225213.

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2000US-0198123.
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CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders c.g. cerebrovascular disorders e.g. cerebral ischaemia, CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and CC angiogenesis, infections caused by bacteria, viruses c.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders c.g. e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders c.g. dysphagia, CC e.g. Acquired infection, gastrointestinal disorders e.g. dysphagia, CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes cand pituitary dwarfism, cancers and disorders at the cellular level e.g. CC leukaemia, disorders e.g. nonallergic rhinitis, renal disorders e.g. cc caute kidney failure and blood related disorders e.g. myocardial conferction. The polypeptides can also be used to aid wound healing and CC epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of polypeptides can also be used as a food additive or preservative to
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2000US-0241808. 2000US-0241809. 2000US-0241826. 2000US-0244617.

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181 TSEELLKHIFXLRER 195
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	51	4	ω	2	щ.	Result No.
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Query Match 100.0%; Score 1428; DB 4; Best Local Similarity 100.0%; Pred. No. 2.1e-134; Matches 271; Conservative 0; Mismatches 0;

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505 35.4 276 2 US-08-552-743-7 505 35.4 276 3 US-09-185-370-7 487.5 34.1 272 2 US-08-852-743-6 487.5 34.1 272 3 US-09-185-370-6 487 34.1 545 2 US-08-935-760-4 486 34.0 268 3 US-09-185-370-2 482 33.8 465 2 US-08-114-555A-2 482 33.8 465 2 US-08-935-760-2 478 33.5 465 3 US-08-114-555A-2 478 33.5 465 3 US-08-159-397A-2 470 32.9 506 1 US-08-369-780-2 470 32.9 506 1 US-08-369-780-2 470 32.9 506 1 US-08-36-036-2 470 32.9 506 1 US-08-636-036-2 470 32.9 506 3 US-08-180-039-2	35.4 276 3 US 34.1 277 3 US 34.1 277 3 US 34.1 272 3 US 34.0 268 3 US 34.0 268 3 US 34.0 268 3 US 33.8 465 2 US 33.8 465 2 US 33.8 544 3 US 33.9 506 1 US 32.9 506 1 US 32.9 506 1 US 32.9 506 1 US 32.9 506 3 US
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3 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	2 US-08-852-743-7 2 US-08-852-743-7 3 Sequence 2 US-08-852-743-6 2 US-08-852-743-6 3 US-09-185-370-6 3 US-09-185-370-6 2 US-08-935-760-4 2 US-08-935-760-4 2 US-08-935-760-2 3 US-08-935-760-2 3 US-08-935-760-2 3 US-08-59-397A-1 3
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US-08-952-743-7 US-09-185-370-7 US-08-952-744-6 US-08-952-744-3 US-08-935-760-4 US-08-935-760-2 US-08-953-760-2 US-08-953-780-2 US-08-559-397A-19	-08 -852-743-7 -08 -852-743-6 -08 -852-743-6 -08 -852-743-6 -09 -185-370-6 -09 -185-370-6 -08 -935-760-4 -08 -935-760-4 -08 -935-760-2 -08 -114-555A-2 -08 -553-37A-1 -08 -559-397A-1 -08 -559

ALIGNMENTS

## US-09-060-410-4 ; MOLECULE TYPE: protein US-09-060-410-4 COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPATION OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/060,410 FILING DATE: 14-APR-1998 CLASSIFICATION: APTORNEY/AGENT INFORMATION: NAME: MAKI, David J. REGISTRATION NUMBER: 31,392 REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 860098.421 TELECOMMUNICATION INFORMATION: THE TENDIANE. 7086 8792-4400 Sequence 4, Application US/09060410 Patent No. 6165461 GENERAL INFORMATION: APPLICANT: Cobb, APPLICANT: Hutchi TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: TYPE: amino acids TOPOLOGY: line WOLECHT ZIP: 98104 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk APPLICANT: Chen, Zhu APPLICANT: Berman, Kevin TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF TITLE OF INVENTION: THEREFOR NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: STREET: 6300 C CITY: Seattle STATE: Washing TELEPHONE: COUNTRY: ADDRESSEE: Washington 7: USA E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue Cobb, Melanie Hutchinson, Michele (206) 622-4900

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US-09-060-410-2
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                                                                                                                              Matches
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Best Local (
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APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson; Michele
APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES AND I
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 8600

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEPHONE: (206) 622-691
                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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             61 KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG 120
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STATE:
75 KEVKFLQRIKHPNSIEYKGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAITHG
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                                                         Local Similarity
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                                                                                                                         Score 1316; DB 4;
Pred. No. 3.6e-123;
17; Mismatches 11;
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                                                                                                                                                                                                Matches 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                         TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                           134 TLDALRYLHSLKRIHRDIKAGNILLSDHAIVKLADFGSASLVDPAQTFIGTPFFMAPEVI
                                        121 ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVI 180
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181 LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPAL-----QSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY:
STATE:
                                                                                    74
                                                                                              61 KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG 120
                                                                                                                                                                                                                                                                             TYPE: amino a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP:
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No. 6165461
                                                                                 KEVSFLNTVVHPHIVDYKACFLKDTTCWLVMEYCIGSAADIVDVLRKGMREVEIAAICSQ 133
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                                                                                                                                                                                                                                                                                                                                                                                                                       David J.
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                                                                                                                                                                                                              59.4%;
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Pred. No. 4e-77;
                                                                                                                                                                                                 Mismatches
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RESULT 4
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APPLICANT: Tyrell E. No. 6034228ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 5
LENGTH: 431
NUMBER OF SEO ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                 Sequence 5, Application US/09340993 Patent No. 6034228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                        APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
FILE REFERENCE: PHM.70296.N1
CURRENT APPLICATION NUMBER: US/09/340,993
CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0 & US
EARLIER FILING DATE: 1997-12-19 & 1998-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tyrell E. NO. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
TITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM. 70296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT FILING DATE: 1998-12-15
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
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SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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46.6%; Pred. No. 2e-50;
46.6%; Mismatches 84;
                                                                                09/211,930
                                                                                                                                                             SERINE/THREONINE KINASE
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US-09-340-993-5
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LENGTH: 431
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Best Local
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Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                            Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN STE20-LIKE STREY TITLE OF INVENTION: SERINE/THREONINE KINAN FILE REFERENCE: PHM.70272

CURRENT APPLICATION NUMBER: US/09/152,406

CURRENT FILING DATE: 1998-09-14

EARLIER APPLICATION NUMBER: 9719920.2

EARLIER FILING DATE: 1997-09-19
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APPLICANT: Tyrell E. No. 6265560ri
APPLICANT: David Shay Silberstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo
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                  --KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE-GNYSKPLK
                                                                                             DYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI-
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US-09-468-442-5
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                                                                                                                                                                                                                                           Sequence 2, Application US/08852743 Patent No. 5830699
GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/340,993
EARLIER FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
EARLIER APPLICATION NUMBER: US 09/211,930
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APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                     APPLICANT: FOTCE, IMPLICANT: FOTCE, JOHN M.
APPLICANT: Kyriakis, John M.
APPLICANT: Pombo, Celia M.
APPLICANT: Bonventre, Joseph
APPLICANT: BONVENTION: SOK-1 AND METHODS OF USE
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                            CORRESPONDENCE ADDRESS:
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                     COUNTRY:
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William Craig Moore
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                                                                                          Fish & Richardson,
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RESULT 9 US-09-211-930-4

GENERAL INFORMATION:
APPLICANT: Tyrell E. No. 5962265ri
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein

5962265ris

Sequence 4, Application US/09211930 Patent No. 5962265

SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4

TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION TITLE OF INVENTION: SERINGTHREONINE KINASE FILE REFERENCE: PHM. 70296
CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT FILING DATE: 1998-12-15
EARLIER FILING DATE: 1997-12-19
EARLIER FILING DATE: 1997-12-19
UNMBER OF SEQ ID NOS: 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016
FILING DATE: 7-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAX: 617/542-8906
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247 VEACLNKDPRFRPTAKELLKHKFITR 272
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                                                                                                                                                                 128 LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 183
                                244 VDSCLQKIPQDRPTSEVLLKHRFVLR 269
                                                                                                         184 DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF 243
                                                                                                                                             131 LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
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FILING DATE: 7-MAY-1997
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SOFTWARE: FastSEQ for Windows Version
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                                                                      KQSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKNSPPTLEGQH-SKPFKEF
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Best Local Similarity
Matches 124; Conserv
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CURRENT FILING DATE: 1999-06-25
EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930
EARLIER FILING DATE: 1997-12-19 & 1998-12-15
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70296.N1
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                                                                DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF 243
                                                                                                       LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
                                                                                                                                                                          CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY 130
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US-09-185-370-2
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                                                                                                                                                                                                                                                                                          Matches 124;
                                                                                                                                                                                                                                                                                                        Best Local Similarity
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APPLICANT: Force,
APPLICANT: Kyriak
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Fraser, Janis K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette
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STREET: __
STREET: __
244 VDSCLQKIPQDRPTSEVLLKHRFVLR 269
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247 VEACLNKDPRFRPTAKELLKHKFITR
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SOFTWARE: FastSEC
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ZIP: 02110-2804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00
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                                                                                                                                                                                                                               15
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                                              KQSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKNSPPTLEGQH-SKPFKEF
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                                                                                                                                                                                                                            DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ 72
                                                                          DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF 243
                                                                                                        LHSERKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
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46.6%;
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                                                                                                                                                                                                                                                                                                       Score 568.5; DB Pred. No. 8e-49;
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                                                                                                                                                                                                                                                                                         85;
                                                                                                                                                                                                                                                                                                                   Length 426;
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                                                                                                        187
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6,

13;

Gaps

6,

243 187

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tyrell E. NO. 6300098ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70296.NI
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: US 09/340.993
EARLIER FILING DATE: 1999-06-25
EARLIER FILING DATE: 1997-12-19
EARLIER FILING DATE: 1997-12-19
EARLIER FILING DATE: 1997-12-19
EARLIER FILING DATE: 1998-12-15
EARLIER FILING DATE: 1998-12-15
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-152-406-4
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TITLE OF INVENTION: SERINE/THREONINE KINASE
FILE REFERENCE: PHM.70272
CURRENT APPLICATION NUMBER: US/09/152,406
CURRENT FILING DATE: 1998-09-14
EARLIER APPLICATION NUMBER: 9719920.2
EARLIER FILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-152-406-4
                       SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09468442 Patent No. 6300098
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Best Local Similarity
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APPLICANT: Tyrell E. No. 6265560ris
APPLICANT: David Shay Silberstein
                                                                 NUMBER OF SEQ ID NOS:
LENGTH: 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK--PGPLEETYIATILREILKGLDY 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.8%; Score 568.5; DB 46.6%; Pred. No. 8e-49;
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; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
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; ORGANISM: H
US-09-468-442-4
                                                                                                                                                                                                                                                                                                                                                                            Query Match 39.0%; Score 557.5; DB 2; Best Local Similarity 45.1%; Pred. No. 9.7e-48; Matches 120; Conservative 46; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: TYTELLE, NO. 5962265ris

APPLICANT: William Craig Moore

APPLICANT: David Shay Silberstein

TITLE OF INVENTION: SETIE/THREONINE KINASE

FILE REFERENCE: PHM. 70296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.8%;
Best Local Similarity 46.6%;
Matches 124; Conservative 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/211,930
CURRENT FILING DATE: 1998-12-15
EARLIER APPLICATION NUMBER: GB 9726851.0
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF
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                                                              CDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLLRA--GPFDEFQIATMLKEILKGLDY 134
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VDSCLQKIPQDRPTSEVLLKHRFVLR 269
                                           QQSAYDSKADIWSLGITAIELAKGEPPNSDMHPMRVLFLIPKNNPPTL-VGDFTKSFKEF
                                                                                                                                                                LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 183
                                                                                                                                                                                                                                                                                              DPEELFTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDL--EEAEDEIEDIQQEITVLSQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEACLNKDPRFRPTAKELLKHKFITR 272
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Pred. No. 8e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 416;
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GENERAL INC. 3702000

GENERAL INC. 3702000

APPLICANT: Tyrell E. No. 5962265ris

APPLICANT: William Craig Moore

APPLICANT: William Craig Moore

APPLICANT: David Shay Silberstein

TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION

TITLE OF INVENTION: SERINE/THREONINE KINASE

FILE REFERENCE: PHM. 70296

CURRENT APPLICATION NUMBER: US/09/211,930

CURRENT FILING DATE: 1998-12-15

EARLIER FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 11

LENGTH: 416

TYPE: PRT

ORGANISM: Mus musculus

US-09-211-930-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-09-211-930-11
; Sequence 11, Application US/09211930; Patent No. 5962265;
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Search completed: November 22, 2002, 12:28:09 Job time: 9.212 secs
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                                                                                                                                                251 IDACLNKDPSFRPTAKELLKHKFIVK
                                                                                                                                                                                                                         135 LHSEKKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI--- 191
                                                                                                                                                                                                                                                   128 LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 183
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                                                                                            77 CDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLLRA--GPFDEFQIATMLKEILKGLDY 134
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Ste20-like protein
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ФР	Qу	дь 04	Db Qy	Фр	Query Best   Match	RESULT 117365 Spec. C:Spec. C:Cpate C:Date C:Acce: A:Refe. A;Refe. A;Refe. A;Rofe. A;Rofe. A;Rofe. A;Rofe. A;Rofe. A;Rofe. A;Rofe.		
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RNFVDSCLQKIPQDRPTSE 	LAMDEGQYDGKVDVWSLGITC	LHSHNMIHRD	)KLRHPNT :::   : )RIKHPNS	CDDPEKLE:	imilarity ; Conserva	protein norveg 199 #seq 165 Berman, 13, 2862 10 of TA 13, 2862 13, 2862 14, 2187 15, 2187 16, 2187 17, 2187 18, 2187 18, 2187 19, 2		30.0 30.1 30.0 30.0 30.0 30.0 30.0 30.0
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VILLE 	CIE	AGNJ AGNJ	CYLF	IGHC	28; 78; 1	se 1 (Noi rev ; CC 32; CC UID: UID:		
RNFVDSCLOKIPQDRPTSEVLLKHRFVLRER 271 	LAMDEGQYDGKVDVWSLGITGIELAERKPPLFNMNAWSALYHIAQNESF 	ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTDYWMAPEV 	KEVRELQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG    :   ::   :	VAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDII :      :	Score 1316; DB 2; Pred. No. 3.6e-59; 7; Mismatches 11;	RESULT 1  T17365  serine/threonine protein kinase TAO1 - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change C;Accession: T17365 R;Hutchison, M.; Berman, K.S.; Cobb, M.H. J. Biol. Chem. 273, 28625-28632, 1998 A;Title: Isolation of TAO1, a protein kinase that activates MEK A;Reference number: Z18730; MUID:99003202; PMID:9786855 A;Reterence number: Z18730; MUID:99003202; PMID:9786855 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1001 <hutd> A;Cross-references: EMBL:AF084205; NID:g3452472; PID:g3452473; C;Function: probably implicated in the regulation of the p38</hutd>	ALIGNMENTS	T38086 S46367 T51417 T696575 T27623 T27623 T27622 T31479 S51884 S51884 S60402 S51884 S
	SPALQSGHWSEYF 240         :   SPTLQSNEWSDYF 254	FVGTPYWMAPEVI 180               	PLQEVEIAAVTHG 120 	SGKQSNEKWQDII 60               SGKQSTEKWQDII 74	Length 1001; Indels 0; Gaps 0;	change 15-Oct-1999 ites MEKs in stress-activated 152473; PIDN:AAC71014.1 the p38-containing stress-res		serine/threonine-p protein kinase CDC protein kinase-lik probable MEK kinas hypothetical prote protein kinase Pak hypothetical prote probable protein k hypothetical prote protein kinase CLA hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

RESULT 2
T18576
T18576
Serine-threonine kinase - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999
C;Accession: T18576
R;Cope, M.J.T.V.; Kendrick-Jones, A.
submitted to the EMBL Data Library, July 1995
A;Reference number: Z18984

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A;Cross-references: (C;Genetics: A;Gene: F23010.20 A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                   A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
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밁
                                                                           Вþ
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-836 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable serine/threonine kinase F23010.20 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U32275; A;Experimental source: strain N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-982 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: T18576
A; Status: prelimina
                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: B96716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: CESP:Sulu
                                                                                                                                                        Matches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status: preliminary; translated
                                                                                                                                                                                               Query Match
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300 QQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVADLMNVTEEALEEYQIAYICREALKGL
                                                                             242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 TLDALRYLHSLKRIHRDIKAGNILLSDHAIVKLADFGSASLVDPAQTFIGTPFFMAPEVI 196
                                      67
                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 162; Conserv
                                                                                                                   7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDII 60
                                                                                               KDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFL 66
                      QKLRHPNTIQYRGCYLREHTAWLYMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPAL-----QSG
                                                                           REDPTTKYEFLNELGKGSYGSVYKARDLKTSEIVAVKVISLT--EGEEGYEEIRGEIEML 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAALFSNKDPEQRYQDLREIGHGSFGAVYFAYDKKNEQTVAIKKMNFSGKQAVEKWNDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EWSLEFVQFIDKCLRKPAEERMSAEECFRHPFIQRSR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAMDEGHYTDRADIWSLGITCIELAERRPPLFSMNAMSALYHIAQNDPPTLSPIDTSEQP
                                                                                                                                                                            Similarity
                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                            GB:AE005173; NID:g7705100; PIDN:AAF67779.1; GSPDB:GN00141
                                                                                                                                                                        44.2%;
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58.5%;
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                                                                                                                                                    Score 631.5; DB 2;
Pred. No. 6.1e-25;
""" matches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 883; DB 2;
Pred. No. 1.8e-37;
8; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P.; Southwick, A.M.; Sun,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.; Khan, S.; Khaykin, Luros, J.S.; Maiti, R.
                                                                                                                                                        Indels
                                                                                                                                                                                           Length
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359
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submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid T1
A;Reference number: 821512
A;Accession: T34356
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                            hypothetical protein T19A5.2 - Caenorhabditis elegans C;SpecLes: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #t. C;Accession: T34356
A; Molecule type: DNA
A; Restdues: 1-653 <BRA>
A; Cross-references: EMBL: U53153; PIDN: AAC69038.1; GSPDB: GN00023; CESP: T19A5.2
A; Experimental source: strain Bristol N2; clone T19A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X99325; NID:g1430821; PIDN:CAA67700.1; PID:g1430822 A;Experimental source: cell type B cell C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Keywords: ATP; autophosphorylation; phosphotransferase; protein kinase; stress-indu F;18-270/Domain: protein kinase homology <KIN>
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R;Pombo, C.M.; Bonventre, J.V.; Molnar, A.; Kyrlakis, J.; Force, T. EMBO J. 15, 4537-4546, 1996
A;Title: Activation of a human Ste20-like kinase by oxidant stress A;Reference number: S71886; MUID:97042345; PMID:8887545
A;Accession: S71886
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A; Residues: 1-426 < POM>
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C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVILAM 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDSCLQKIPQDRPTSEVLLKHRFVLR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKNSPPTLEGQH-SKPFKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 127
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                                                                                                                                                                                                                                                      #sequence_revision 29-Oct-1999 #text_change
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R;Bentley, D.; Le, T.T.

submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid ZC404.
A;Reference number: Z20614
A;Reference number: Z20614
A;Reference number: Z20614
A;Reference number: Z20614
A;Recssion: T29372
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-829 <BEN>
A;Cross-references: EMBL:U55363; PIDN:AAA97966.1; GSPDB:GN00023; CESP:ZC404.9
A;Cross-references: EMBL:U55363; PIDN:AAA97966.1; GSPDB:GN00023; CESP:ZC404.9
A;Experimental source: strain Bristol N2; clone ZC404
C;Genetics:
A;Gene: CESP:ZC404.9
A;Map position: 5
A;Introns: 36/2; 82/2; 103/1; 131/3; 520/3; 622/2; 796/2
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
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A;Gene: CESP:T19A5.2
A;Map position: 5
A;Introns: 26/3; 101/3;
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H-WSEYFRNFVDSCLQKIPQDRPTSEVLL-KHRFVL 268
                                                                                                                                                                                                                               EVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHG 120
                                                                                                                                                                                                                                                                                                               EFVEMCLNKDPENRPSASTLLKHQFIKRAK 289
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                                      PEVACVEKRGGYGMQCDVWATGITAIELGECQPPLFDLHPMQVLYLMTKSGYKPPHLKDK
                                                                           PEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN--ESPALQSG 234
                                                                                                                    TLRGLNYLHNMGKIHRDIKGANILLSSSGDVKLADFGVAAQITATIGKRKSFIGTPYWMA
                                                                                                                                                                                                     EIMVIRECSHPNIIAYFGSYIRRDRLWIVMEYCGGGSLQDIYHL-TGPLSELQIAFVCRE 118
                                                                                                                                                                                                                                                                                     ADVIKRSNPADDYELLQRVGSGTYGEVYKARDIRSDSLAAVKVVKL---EAGDNFAVIQQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KQSSYDYKADIWSLGITAIELANGEPPHSDLHPMRVLFLIPKNPPPVLQGSQWSKPFK
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43.0%;
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                                                                                                                                                                                                                                                                                                                                                                                             Score 527.5; DB 2; Pred. No. 9.8e-20;
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Pred. No. 2.1e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            kinase
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                                                                                                                                                                                                                                                                                                                                                                         7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            homo]
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Cross-references: GB:U07349; NID:g531819; PIDN:AAA20968.1; PID:g531820 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; prote: C;Keywords: ATP; phosphotransferase
                                                                                                                     R;Katz, P.; Whalen, G.; Kehrl, J.H.
J. Biol. Chem. 269, 16802-16809, 1994
A;Title: Differential expression of a novel
A;Reference number: A53714; MUID:94266900; i
A;Accession: A53714
                                                                                                                                                                                                                                                                  protein kinase (EC 2.7.1.37)
N;Alternate names: GC kinase
C;Species: Homo sapiens (man
                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-819 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein F12M16.4 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96572
                                                                                                                                                                                                                          C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change
C;Accession: A53714
                                                                                                                                                                                                                                                                                                                                                                                                                    В
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A; Residues: 1-690 <S
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                                                                                                                                                                                                                                                                                                                                                      RESULT 8
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                                                                                                                                                                                                                                                                     Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: F12M16.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 FSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIK -----EV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                       YFRNFVDSCLQKIPQDRPTSEVLLKHRFVLRER
                                                                                                                                                                                                                                                                                                                                                                                                                  PLKEFVSFCLKKAPAERPNAKELLKHRFIKNAR 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAVEYLHAEGKIHRDIKAANILLSENGDVKVADFGVSAQLTRTISRRKTFVGTPFWMAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRWTPLFHDFVRQCLTKNPKKRPSPEKLLTSHPFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VI-QNSEG-YNEKADIWSLGITMIEMAKGEPPLADLHPMRVLF-IIPRESPPQLDEHFSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVLSQCRCPYITEYYGSYLHQTKLWIIMEYMAGGSVADLLQ-PGNPLDEISIACITRDLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RFLQKLRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGAL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSQFELIGRGSFGDVYKAFDTELNKDVAIKVIDL--EESEDEIEDIQKVSLELTLVLLEI 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-690 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.9%; Score 512.5; DB 2
43.6%; Pred. No. 4.7e-19;
                                                                                                                                                                                                                                                                                                             BL44
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Conway, A.B.; Conv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                           l protein kinase
PMID:7515885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSPDB: GN00141
                                                                                                                                                                                                                                                 24-Sep-1999
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                   protein
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Maiti, R.; Marzia
                                                                                                                                                                B lymphocytes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: msn
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: third instar eye-antennal disk cosmid library A; Note: the cited accession number, 1076485, is not in Genbank release 111.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-1102 < TRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: JC6316; A; Accession: JC6316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: misshapen encodes a protein kinase involved in A;Reference number: JC6316; MUID:97199378; PMID:9047354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: JC6316
R; Treisman, J.E.; Ito, Gene 186, 119-125, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                      Match 35.7%; Score 510.5; DB;
Local Similarity 41.5%; Pred. No. 8.9e-19;
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                                                                                                                                       SKKWSKKFHGFIDTVLVKDYHQRPYTENLLKHGFI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRHPNVVAYIGSYLRNDRLWICMEFCGGGS--LQEIYHATGPLEERQIAYVCRERLKGLH 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
                                                                                                                                                                                                                                     L-RHPNTIQYRGCYL-----REHTAWLYMEYC-LGSASDLLEVHK-KPLQEVEIAAVTH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APEVI - ACDENPOATY DNRSDLWSLGITALEMAESQPPLCDLHPMRALFLIPRNSPPRLK
                                                                                                        APEVILAMDE - - - GQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQ 232
                                                                                                                                                                                                                                                                                                                      DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERKGGYNELCDVWALGITAIELGELQPPLFHLHPMRALMLMSKSSFQPPKLRDKTRWTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKK--PLQEVEIAAVTHGALQGLA 126
                                 SGHWSEYFRNFVDSCLQKIPQDRPTSEVLLKHRFV 267
                                                                                                                                                                                                               YSNHRNIATYYGAFIKKSPPGKDDQLWLVMEYCGAGSVTDLVKSTKGQSLKEEWIAYICR 142
                                                                                                                                                                                                                                                                                   DPAGIFELIEVVGNGTYGQVYKGRHTKTGQLAAIKVMDV----TEDEEEEIKLEINVLKK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFRNEVDSCLQKIPQDRPTSEVLLKHRFVLRE 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLHSHNMIHRDVKAGNILLSEPGLVKLGDFG-----SASIMAPANSFVGTPYWMAPEVIL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPRDRFELLQRVGAGTYGDVYKARDTVTSELAAVKIVKL---DPGDDISSLQQEITILRE
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41.2%;
                                                                                                                                                                                                                                                                                                                                                         54; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 511; DB 2; Pred. No. 6.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275
                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                           86;
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                                                                                                                                                                                                                                                                                                                                                                                        Length 1102;
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RESULT 11
T34021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Itoh, S.; Kameda, Y.; Yamada, E.; Tsujikawa, K.; Mimura, T.; Kohama, Y. Arch. Biochem. Biophys. 340, 201-207, 1997
A;Title: Molecular cloning and characterization of a novel putative STE20 A; Reference number: Z18952; MUID:97288344; PMID:9143322
A; Accession: T18532
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                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T34021
R;Fukami, Y.; Yamamoto, H.; Ichihara, T.; Mori, K.; Gomi, T.; submitted to the EMBL Data Library, April 1997
A;Description: SK2, a putative rat homologue of yeast protein A;Reference number: Z21463
A;Accession: T34021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein kinase SK2 - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1231 <ITO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Cavia porcellus (guinea pig)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jul-2000
C;Accession: T18532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine/threoine protein kinase - gui N;Alternate names: STE20-like kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T18532
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Best Local Similarity
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Local Similarity 39.9%; Pred. No. 2.5e-18;
86
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CDHPNIVKLLDAFYYENNLWILIEFCAGGAVDAVMLEL-ERPLTESQIQVVCKQTLEALN 144
                 LRHPNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKPLQEVEIAAVTHGALQGLA 126
                                                                         NPEEFWEIIGELGDGAFGKVYKAONKETNVLAAAKVID---TKSEEELEDYMVEIDILAS 85
                                                                                                           DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRNEVDSCLQKIPQDRPTSEVLLKHRFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPEEFWETIGELGDGAFGKYYKAQNKETNYLAAAKVID---TKSEEELEDYMYEIDILAS 85
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39.9%;
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                                                                                                                                                                       Score 500.5; DB 2; Pred. No. 3e-18;
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A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-1233 <SUY A;Cross references: EMBL:U88984; hC;Keywords: protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
T14157
                                                                                                                                                             serine/threonine protein kinase NIK - mouse
N;Alternate names: Nck interacting kinase
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change
C;Accession: T30989
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                                                                                                        R;Su, Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y. EMBO J. 16, 1279-1299, 1997 EMBO J. 16, 1179-1299, 1997 A;Title: NIK is a new Ste20-related kinase that binds NCK and A;Reference number: Z20954; MUID:97280817; PMID:9135144
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A; Residues: 1-1233 < PYT>
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                                      EMBL: U88984; NID: g1872545; PID: g1872546; PIDN: AAC53165
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Pred. No. 3.9e-18;
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p21-activated protein kinase - human C;Species: Homo sapiens (man) C;Date: 21-Dec-196 #sequence_revisicC;Accession: G01773
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            #sequence_revision
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R;Manser, E; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.

R;Manser, E; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.

R;Manser, E; Leung, T.; Salihuddin, H.; Zhao, Z.; Lim, L.

A;Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.

A;Reference number: $40482; MUID:94150588; PMID:8107774

A;Recession: $40482

A;Accession: $40482

A;Molecule type: mRNA

A;Residues: 1-544 <MAN>

C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F;267-520/Domain: protein kinase homology <KIN>

F;275-283/Region: protein kinase ATP-binding mottif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        serine/threonine-specific protein kinase (EC 2.7.1.-) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S40482
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Best Local Similarity
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                                                        FVDSCLQKIPQDRPTSEVLLKHRFV 267
                                                                                                                                                                                                                                                                                                                                          NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALEF
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                                                                                                                                                                   DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN 242
                                                                                                                                                                                                                               LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV--- 435
                                                                                                                                                                                                                                                                                     LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM 183
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FLNRCLEMDVEKRGSAKELLQHQFL
                                                                                                                 TRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRD
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Pred. No. 4.1e-1
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06-Jun-1997

#text\_change

24-Sep-1999

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R:Chernoff, J.

Submitted to the EMBL Data Library, April 1995

A:Reference number: G08374

A:Accession: G01773

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-545 <CHE>
A:Cross-references: EMBL:U24152; NID:g780805; PIDN:AAA65441.1; PID:g780806
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A;Gene: Pak1
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
F;268-521/Domain: protein kinase homology <KIN>
Search completed: November 22, 2002, 12:27:27 Job time: 11.588 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 34.3%; Score 490; DB 2; Length 545; Best Local Similarity 42.3%; Pred. No. 5.2e-18; Matches 112; Conservative 46; Mismatches 93; Indels 14; Gaps
                                                                                                                                          497 FLNRCLDMDVEKRGSAKELLQHQFL 521
                                                                                           243 FVDSCLQKIPQDRPTSEVLLKHRFV 267
                                                                                                                                                                                                               265 DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE 321
                                                                                                                                                                                                                                                                                                                                                                                     9 DPEKLFSDLREIGHGSFGAVYFÄRDVRNSEVVÄIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
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Result
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version (c) 1993 - 2002
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                                                                                                                                                          MI15_CAEEL
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Q13153
P08458
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Q13188
P35465
                                                             Q12469
Q9uew8
Q88506
                     Q9z1w9
P48562
                                                                                                                                 Q23356
096013
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P50527
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Q64303
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homo sapien
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62/4 62/6 1401 1401 1402 1403 1403 1403 1403 1403 1403 1403 1403	9/4 1 CCLb_YEAST P2/65/626 1 M3K3_HUMAN 099/59 1401 1 WIS4_SCHPO 014299 1401 1 WIS4_SCHPO 014299 1401 1 WIS4_SCHPO 011399 1408 1 M3K3_MOUSE 011389 1501 1 NINC_DROME 0106/6 1501 1 NINC_DROME 0106/6 1619 1 M3K2_HUMAN 061083 1493 1 M3K1_RAT 062925 1493 1 M3K1_HUMAN 052925 1579 1 SSKK_YEAST P53349
	1 M3K3_HUMAN 1 W1S4_SCHPO 2014299 1 W1S4_SCHPO 2014299 1 W1S4_SCHPO 2014299 1 M3K3_MOUSE 201389 1 NINC_DROME 201389 1 NINC_DROME 201389 201389 201389 201389 201389 201389 201389 201389 201381
L CCLL YEAST L CAST THOMAN L WIS4_SCHPO L WI	P2/65 P2/95 Q99/59 Q61084 Q61084 Q01389 P53349 P53359
CCLD_YEAST WIS4_SCHPO WIS4_SCHPO M3K3_MOUSE BCKL_YEAST NINC_DROME M3K2_MOUSE M3K2_MOUSE M3K1_RAT M3K1_RAT M3K1_HUMAN M3K1_HUMAN M3K1_HUMAN M3K1_MOUSE SKK2_YEAST	P2/65 P2/95 Q99/59 Q61084 Q61084 Q01389 P53349 P53359
	P2/636 Q99759 Q14299 Q14299 Q01389 P10676 Q992U5 Q61083 Q62925 P53349

## ALIGNMENTS

RESULT 1 SULU\_CAEEL

SULU\_CAEEL STANDARD; PRT; 982 AA.

P46549;
10.-NOV-1995 (Rel. 32, Created)
11.-OCT-2001 (Rel. 40, Last sequence update)
11.-OCT-2001 (Rel. 40, Last annotation update)
25 Serine/threenine-protein kinase SULU (EC 2.7.1.-).
27 KIN-18 OR SULU OR T17E9.1.
28 Caenorhabditis elegans.
29 Caenorhabditis elegans.
20 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
20 NOBI\_TaxID=6239;

Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

SEQUENCE FROM N.A. STRAIN-Bristol N2;

SEQUENCE FROM N. Submitted (JUN-1994)

to the

EMBL/GenBank/DDBJ databases

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STITION OF THE TREATMENT OF THE TREATMEN
   Query Match
Best Local Sim
Matches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U11280; AAA19437.1; -
EMBL; U32275; AAA75370.1; -
WormPep; T17E9.1; CE01405.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000290; Ser_thr_pkinase.
Dfam. PF00069; pkinase; 1.
                                                                                                                                  PROSITE; PROTEIN_KINASE_ATP; 1.

PROSITE; PSO0107; PROTEIN_KINASE_DATP; 1.

PROSITE; PSO0101; PROTEIN_KINASE_DT; FALSE_NEG.

PROSITE; PSO0108; PROTEIN_KINASE_T; FALSE_NEG.

Transferase; Serine/threonine-protein kinase; ATP-bindir
DOMAIN
30 289 PROTEIN KINASE.

NP_BIND
36 44 ATP (BY SIMILARITY).

BINDING
36 49 ATP (BY SIMILARITY).

ACT_SITE 153 153 BY SIMILARITY.

SEQUENCE 982 AA; 112870 MW; 745CELE2F890977D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_EKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                       Similarity
   Conservative
                                    61.8%;
58.5%;
   48;
                                    Score 883; 1
   Pred. No. 5.36
B; Mismatches
                                    DB 1;
.3e-63;
                                                                                                                                                                                                                                                                                                                    ATP-binding.
                                                                 Length 982;
   Indels
   6
Gaps
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Qy

1 VAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDII 60

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RESULT 2
ST24_HUMAN
STANDARD; PRT; 443 AA.

ID ST24_HUMAN
STANDARD; PRT; 443 AA.

AC Q9Y6E0; O14840;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase 24 (EC 2.7.1.37) (STANDARD)
DE Serine/threonine protein kinase 24 (EC 2.7.1.37) (STANDARD)
DE SERINE/THEORIES (MARTHALE)
DE MST3) (MST-3) (Mammalian STE20-like protein kinase
GN STK24 OR MST3 OR STK3.
     QΥ
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-9801249; PubMed=9353338; Schinkmann K., Blenis J.;
                                                                                  This
                                                                                                                                                                                                                                                                                                                                                             Zhou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                    between
                                                                                                                                                                                                                  ---
                                                                                                                                                                                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                                                                                      STE20-like kinase 3 that is
                                                                                                                                                                                                                                                                                                                                                  Pei
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20112812;
                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM B), AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and characterization of a human with unusual cofactor requirements.";
J. Biol. Chem. 272:28695-28703(1997).
                                                                                                                                                                                                                                                                                                         kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                    "Identification of a human brain-specific isoform of mammalian STE20-like kinase 3 that is regulated by cAMP-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235
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                                                                                                                                                                                     SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE);
PRODUCED BY ALTERNATIVE SPLICTING.
TISSUE SPECIFICITY: ISOFORM A IS UBIQUITOUS. ISOFORM B 1
                                                                                                                                                                                                                                         CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein COFACTOR: ISOFORM A REQUIRES MANGANESE FOR ITS ACTIVITY.
                                                                                                                      SIMILARITY: BELONGS
                                                                                                          STE20 SUBFAMILY.
                                                                                                                                                PTM: AUTOPHOSPHORYLATED. ISOFORM B
                                                                                                                                                               CEREBRAL CORTEX
                                                                                                                                                                         EXPRESSED IN BRAIN WITH HIGH EXPRESSION IN
                                                                                                                                                                                                                                                                     RESIDUES
                                                                                                                                                                                                                                                                                 FUNCTION:
                                                                SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                             Chem.
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PROTEIN KINASE THAT !
                                                                                                                                                                                                                                                                                                                                                                        PubMed=10644707;
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                                                                                                                      TO
                                                                                                                      THE
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                                                                                                                      SER/THR FAMILY
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                                                                             It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STE20-like
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                                                                  EMBL outstation
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Query Match
Best Local
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                                                                                                                       Serine/threonine protein kinase 25 (EC 2.7.1.37) stress response kinase 1) (Ste20/oxidant stress r (SOK-1) (Ste20-like kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MUTAGEN
CONFLICT
STRAIN-C57BL/6J;
Melnick M.B.;
                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                          Q9Z2W1;
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINA;
                              SEQUENCE FROM
                                                                         Mammalia;
                                                                                     Eukaryota;
                                                                                                     Mus musculus (Mouse)
                                                                                                                    STK25 OR SOK1.
                                                                                                                                                                                                                                       ST25_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew; HGNC:11403; STK24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF024636; AAB82560.1;
EMBL; AF083420; AAD42039.1;
HSSP; P24941; 1CKP.
                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069;
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                                                                                                                                                                                                                                                                                                               ||::|| | | |||:: ||||:||
EFVEACLNKEPSFRPTAKELLKHKFILR
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                                                                                                                                                                                                                                                                                                                                           NFVDSCLQKIPQDRPTSEVLLKHRFVLR
                                                                                                                                                                                                                                                                                                                                                                        --KQSAYDSKADIWSLGITAIELARGEPPHSELHPMKVLFLIPKNNPPTLE-GNYSKPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                DYLHSEKKIHRDIKAANVLLSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KADPEELFTKLEKIGKGSFGEVFKGIDNRTQKVVAIKIIDL--EEAEDEIEDIQQEITVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604984;
                                                                                                                                                                                                                                                                                                                                                                                                  AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYWMAPEVIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00108; PROTEIN_KINASE_ST; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000719; Euk_pkinase.
IPR002290; Ser_thr_pkinase.
IPR001245; Tyr_pkinase.
0069; pkinase; 1.
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414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĀΑ;
                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN_KINASE_ATP;
                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49307
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46.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY).

BY SIMILARITY (BY PRA).

PHOSPHORYLATION (BY PRA).

PHOSPHORYLATION (BY PRA).

MDSRAQLWGLALNKRRATLPHPGGST -> M.

GMQ (IN ISOFORM A).

T->A: LOSS OF PHOSPHORYLATION BY

A -> V (IN REF. 2).
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Pred.
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                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4A9FF1F6B6A88A97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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No. 1.5e-39;
                                                                                                                                                                                          update)
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                                                                                                                                                response kinase-1)
                                                                                                                                                            (Sterile
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                                                                        Euteleostomi;
; Murinae; Mus
                                                                                                                                                            20/oxidant
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RESULT 4
ST25_HUMAN
ID ST25_H
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Best Local :
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Phosphorylation.
DOMAIN 20
NP_BIND 26
NP_BIND 49
  ST25_HUMAN S
000506; Q15522;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
16-OCT-2001 (Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genetic mapping of human and mouse PAK genes.";
Submitted (MAY-1997) to the EMBL/GenBank/DDB/ databases.
-!- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE
MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000001; Euk_pkinase; 1.
SMARF; SM00220; S_TKC; 1.
PROSITE; PS001008; PROTEIN_KINASE_ST; FALSE_NEG.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1891699; Stk25.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF004934; AAD01208.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic (By similarity) SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTOPHOSPHORYLATION. THE C-TERMINAL THE KINASE ACTIVITY (BY SIMILARITY).
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                                                                                                                                                  VDSCLQKIPQDRPTSEVLLKHREVLR
                                                                                                                                                                                                                                                                LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPA----NSFVGTPYMMAPEVILAM
                                                                                                                                                                                                                                                                                                                                LRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 127
                                                                                                                                  VEACLNKDPRFRPTAKELLKHKFITR
                                                                                                                                                                                        KQSAYDFKADIWSLGITAIELAKGEPPNSDLHPMRVLFLIPKNNPPTLE-GHHSKPFKEF
                                                                                                                                                                                                             DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYFRNF
                                                                                                                                                                                                                                               LHSERKIHRDIKAANVLLSEQGDVKMADFGVAGQLTDTQIKRNTFVGTPFWMAPEVI---
                                                                                                                                                                                                                                                                                                       CDSPYITRYFGSYLKSTKLWIIMEYLGGGSALDLLK---PGPLEETYIATILREILKGLDY
                                                                                                                                                                                                                                                                                                                                                                DPEELFTKLDRIGKGSFGEVYKGIDNHTKEVVAIKIIDL--EEAEDEIEDIQQEITVLSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                          124;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140
426
(Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
48175 MW;
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34
49
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 572.5; DB 1 Pred. No. 1.3e-38;
                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6A01916034E26362 CRC64;
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                                                                                                                                                             269
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ng as its content
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Query Match
Best Local
     Matches
                                                                                              Phosphorylation
DOMAIN 20
NP_BIND 26
NTNDING 49
                                                                      ACT_SITE CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "YSK1, a novel mammalian protein kinase structurally related and SPS1, but is not involved in the known MAPK pathways."; Oncogene 14:2047-2057(1997).

-i - FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KIND MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=97042345; PubMed=8887545;

Pombo C.M., Bonventre J.V., Molnar A., Kyriakis J., Force T.;

"Activation of a human Ste20-like kinase by oxidant stress defines novel stress response pathway.";

EMBO J. 15:4537-4546(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant stress response kinase 1) (Ste20/oxidant stress response kinase-1) (SNC-1) (Ste20-11ke kinase).
                                                                                                                                                                 PROSITE; PS00108; PROTEIN_KINASE_ST; PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                    EMBL; X99325; CAA67700.1;
EMBL; D63780; BAA20420.1;
HSSP; P12931; 1FMK.
                                                           SEQUENCE
                                                                                                                                                                                                       ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                           or send
                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                      Transferase;
                                                                                                                                                                                                                                     Pfam; PF00069;
                                                                                                                                                                                                                                                InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkir
                                                                                                                                                                                                                                                                              MIM; 602255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97304522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic.
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND
HEART AND LUNG.
SIMILARITY: BELONGS TO THE SER/TH FEAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein. ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STE20 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE KINASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.-I.,
                                                                                                                                                                                                                                                                                      HGNC:11404; STK25
                                                                                                                                                                                                                                                                                                                                                           an email to license@isb-sib.ch).
                Similarity
                                                            426
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Izawa
                                                                                                                                                   Serine/threonine-protein
                                                                                                                                                                                                                                   pkinase;
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49
140
348
48111
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Primates;
                  39.8%;
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                                                                                                                                                                                                                                               thr_pkinase
                                                           Œ.
  44;
Score 568.5; DB 1, Pred. No. 2.7e-38;
                                                                    PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
EP -> DA (IN REF. 1).
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Catarrhini;
                                                         P -> DA (IN REF. 1).
183CE5700FCEA716 CRC64;
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                                                                                                                                                   kinase;
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                                                                                                                                                     ATP-binding;
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STOMACH
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                             Length
    Indels
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                              426;
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  Gaps
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RESULT 5
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EMBL; U18297; AAA83
EMBL; U60207; AAB17
EMBL; AL109839; CAB
HSSP; P24941; 1HCL.
Genew; HGNC:11408;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-96413604; Paylor L.K., Wang H "Newly identified s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Serine/threonine protein kinase 4 (EC 2.7.1.37) (STE20-like kinase MST1) (MST-1) (Mammalian STE20-like protein kinase 1)
(Serine/threonine protein kinase Krs-2).
STK4 OR MST1.
                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein
-!- ENZYME REGULATION: THE C-TERMINAL NON-CATALYTIC REGION INHIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to Ste20.
J. Biol.
                                                                                       the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Creasy C.L., Chernoff J.; "Cloning and characterization of a human to steep".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95394929; PubMed=7665586; Creasy C.L., Chernoff J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-435 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 Laird
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                                                                                                                                                                                                                               ENZYME REGULATION: THE C-TERMINAL NON-CATALYTIC REGION IN THE KINASE ACTIVITY.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
PIM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINA
                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chem.
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                                                AAA83254.1; -.
AAB17262.1; -.
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                                CAB89421.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=8816758;
H.C., Erikson R.L.;
stress-responsive p
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    STK4
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RESULT 6
STK3_HUMAN STANDARD; PRT; 491 AA.

ID STK3_HUMAN STANDARD; PRT; 491 AA.

AC Q13188; Q15801; Q15445;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-CCT-2001 (Rel. 40, Last sequence update)

DT 16-CCT-2001 (Rel. 40, Last annotation update)

DE Serine/threonine protein kinase 3 (EC 2.7.1.37) (STE20-like MST2) (MST-2) (Mammalian STE20-like protein kinase 2)

DE (Serine/threonine protein kinase Krs-1).
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Best Local S
Matches 115
                                                          Gene
                                                                   Creasy C.L., Chernoff J.; "Cloning and characterization of a Ste20-like kinases.";
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Pfam; PF0
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
DOMAIN
                                                                                                      MEDLINE=96144292; PubMed=8566796;
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                        STK3 OR MST2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00059; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
                                                                                                                                          NCBI_TaxID=9606;
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                                                          167:303-306(1995).
                                                                                                                                                                                                                                                                                                                                                                      VDSCLQKIPQDRPTSEVLLKHRFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAPANSFVGTPYWMAPEVILAMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DSPHVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKTLTEDEIATILQSTLKGLEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAYL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQKL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               604965;
                                                                                                                                                                                                                                                                                                                                                VKQCLVKSPEQRATATQLLQHPFV
                                                                                                                                                                                                                                                                                                                                                                                             EIGYNCVADIWSLGITAIEMAEGKPPYADIHPMRAIFMIPTNPPPTFRKPELWSDNFTDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 550; DB 1;
Pred. No. 9.6e-37;
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                                                                               subfamily
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                                                                                of.
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Taylor L.K., Wang "Newly identified

stress-responsive PubMed=8816758; H.C., Erikson R.L.;

protein kinases,

Krs-1

and

MEDLINE=96413604; SEQUENCE FROM

N.A.

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Best Local
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CONFLICT
CONFLICT
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PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.";
Proc.
[3]
                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Euk_pkinase; SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schultz S.J., Nigg E.A.;
Schultz S.J., Nigg E.A.;
"Identification of 21 novel human protein kinases, including 3 members of a family related to the cell cycle regulator nimA of Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U26424; AAC50386.1; -.
EMBL; U60206; AAB17261.1; -.
EMBL; Z25422; CAA80909.1; -.
HSSP; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                           Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069;
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InterPro; IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94100173; PubMed=8274451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                DOMAIN
                          129
   138
                                                                                                                                              Local Simhes 114;
                                                 78
                                                                       70
                                                                                              23
                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELULAR LOCATION: Cytoplasmic (By similar TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS SKELETAL AND PLACENTA TISSUES AND AT VERY LOW HEARF, LUNG AND BRAIN TISSUES.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF STE20 SUBEAMITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Growth Differ. 4:821-830(1993). FUNCTION: OXIDANT STRESS-ACTIVATED MAY PLAY A ROLE IN THE RESPONSE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    605030;
HFMRKIHRDIKAGNILLNTEGHAKLADFGVAGQLTDTMAKRNTVIGTPFWMAPEVI---Q
                      HSHNMIHRDVKAGNILLSEPGLVKLGDFGSA----SIMAPANSFVGTPYWMAPEVILAMD
                                              DSPYVVKYYGSYFKNTDLWIVMEYCGAGSVSDIIRLRNKTLIEDEIATILKSTLKGLEYL
                                                                     RHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGLAYL 128
                                                                                           PEEVFDVLEKLGEGSYGSVFKAIHKESGQVVAIKQVPV----ESDLQEIIKEISIMQQC
                                                                                                                   PEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGNC:11406; STK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                         Similarity
                                                                                                                                                                                            491 AA;
                                                                                                                                               Conservative
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33
36
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146
308
370
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121
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303
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                                                                                                                                                                                                                                                                                                                                        Serine/threonine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                  pkinase;
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41
56
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98
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203
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                                                                                                                                                      37.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Euk_pkinase
                                                                                                                                                                                            MW;
                                                                                                                                            44;
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BY SIMILARITY.
POLY GLU.
POLY-GLU.
WIV -> YLY (IN
D -> Y (IN REF.
                                                                                                                                           Score 538; DB 1;
Pred. No. 8.8e-36;
4; Mismatches 92;
                                                                                                                                                                                                       GEC
                                                                                                                                                                                                                 P -> G
                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93:10099-10104(1996).
                                                                                                                                                                                           EC -> ESV (IN REF. 2).
9CA3B0644F3C14A9 CRC64;
                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                                               (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERINE/THREONINE KINASE THAT ENVIRONMENTAL STRESS (BY
                                                                                                                                                                                                                 REF.
                                                                                                                                                                                                                 (IN REF. REF. 3).
REF. 3).
REF. 2).
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similarity).
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                                                                                                                                                                   Length
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                                                                                                                                           Indels
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                                                                                                                                                                    491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
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                                                                                                                                           14;
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                                                                                                                                          Gaps
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                       184
                                                                                              77
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RESULT 7

PARAL_RAT

ID PARAL_RAT

ID PARAL_RAT

ID PARAL_RAT

ID PARAL_RAT

DT 15-J

DT 15-J

DT 15-J

DE Kina

GN PARI

GN PARI

GN PARI

GN PARI

GN RAT

RA MADI

RR RA MADI

RR REV REV

RR RA Zha

RR RESOR

RR RE
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAKI_RAT STANDARD; PRT; 544 AA.

P35465; Q62934;

01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated kinase 1) (PAK-1) (P68-PAK) (Alpha-PAK) (Protein kinase MUK2).
                                                                   use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restricted by the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96027610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohno S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2hao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase (PAK) family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manser E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 367:40-46(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Racl."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manser E., Leung T., Salihuddin H., Zhao Z.-S., Lim L.;
"A brain serine/threonine protein kinase activated by Cdc42 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Manser E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning of a new member of the p21-Cdc42/Rac-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
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                                                                                                                                                                                                                                                                                                                    GTPASES TO THE JNK MAP KINASE PATHWAY.

SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RAC1 (BY SIMILARITY IN THE BRAIN, TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BRAIN, HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH MOTOI FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.

DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTI EXPRESSION ELSEWHERE.

PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 270:25070-25078(1995).

FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY
LIKELY TO BE THE GTPASE EFFECTOR THAT LIKKS THE
                                                                                                                                                                                                                                                                          SIMILARITY:
                                                                                                                                                                                                                                                                                                    STE20 SUBFAMILY
U23443;
U49953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKKCLVKNPEQRATATQLLQHPFI 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JUL-1996)
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AAB95646.1;
AAB61533.1;
                                                                                                                                                                                                                                                                          CONTAINS 1 CRIB DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=7559638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Т.,
                                                                                                                                     There are no rest
                                                                                        http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michael G., Hall C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suzuki A.,
                                                                                                                        Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BUT NOT GDP-BOUND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIETY OF TARGETS
THE RHO-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                    CNS WITH LITTLE
                                                                                                                                                                                                                                                                                                                           PROTEIN KINASES
                                                                                                                        ру
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                                                                                                                                                                       restrictions
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                                                                                                                        and
                                                                                                                                                                                                 EMBL outstation
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                                                                                                                                                                                                   collaboration - 
L outstation -
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PAK1_MOUSE
ID PAK1_MOUSE
AC O88643;
DT 15-DEC-1998
DT 15-DEC-1998
DT 15-DUN-2002
DE Serine/three
DE kinase 1) (I
DE PAKA OR PAKI
OR PAKI OR PAKI
OR WIS MUSCULUE
OR EUKARYOTA; 1
OC MAMMALIA; ES
OX NCBI_TAXID=
RN [1]
RP SEQUENCE FRR
RX MEDLINE-9921
RA BUTDELO P.D
RT "Cloning, control
RA Gene 232:200
CC -1-FUNCTIO
CC LIKELY'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 112;
                                                                                                                                                              OB8643;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-)
kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK) (CDC42/RAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
BINDING
ACT_SITE
                                 SEQUENCE FROM N.A.

MEDLINE-99282526; PubMed-10352232;

Burbelo P.D., Kozak C.A., Finegold A.A., Hall

"Cloning, central nervous system expression are
the mouse PAK-1 and PAK-3 genes.";
                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prodom; PD000001; Euk_pkinase; 1.

SMART; SM00285; PBD; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS50108; CRIB; 1.

PROSITE; PS50107; PROTEIN_KINASE_ATP; 1

PROSITE; PS00108; PROTEIN_KINASE_DW; 1

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !ransferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000995; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                             496
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  FUNCTION:
LIKELY TO
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; P24941;
                            232:209-215(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                       LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                            FLNRCLEMDVEKRGSAKELLQHQFL 520
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                                                                                                                                                                                                                                                                                                                                                                                                                           LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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269
275
298
388
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  THE ACTIVATED BE THE GTPASE
                                                                                                                                                                                                                                                                STANDARD;
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520
283
298
388
                                                                                                                          Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.5%;
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  EFFECTOR
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LINKER
PROTEIN KINASE.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 492;
                                                                                                                                                                                                                                                               PRT;
                                                                                                                        Craniata; Ver
Sciurognathi;
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ACTS ON A VAI
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                                                                                                                                                                                                                                                                545
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                                                                                                                           Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Mus
              ON A VARIETY
                                                                                                                                                                                                                                                               A
                                                ll A., Pirone D.M.;
and chromosomal mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92;
  THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                      (p21-activated effector kinase
  RHO-RELATED
               QF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544;
              TARGETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                  RESULT 9
PAK1_HUMAN
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PAK1_HUMAN STAN
Q13153; Q13567;
Q1-NOV-1997 (Rel. 3
Q1-NOV-1997 (Rel. 3
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Best Local
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DOMAIN 75
DOMAIN 134
NP_BIND 276
BINDING 296
BINDING 296
ACT_SITE 389
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BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRODOM; PD000001; Euk_pkinase; 1.

SMART; SM00285; PBD; 1.

SMART; SM00220; STKc; 1.

PROSITE; PS50108; CRIB; 1.

PROSITE; PS50107; PROTEIN_KINASE_ATP; 1

PROSITE; PS500108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; 1. Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTPASES TO THE JNK MAP KINASE PATHWAY (BY
-1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND
CDC42/P21 AND RAC1 (BY SIMILARITY).
-1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY
SIMILARITY).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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-!- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
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                                        FVDSCLQKIPQDRPTSEVLLKHRFV
                                                                                                                                                                                                                                                                                                            DPKKKYTPFEKIGQGASGTVYTAMDVATGQEVAIKQMNL---QQQPKKELIINEILVMRE
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FLQCCLEMDVEKRGSAKELLQHQFL
                                                                                                   TRKAYGPKVDIWSIGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRD
                                                                                                                              DEGQYDGKYDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYFRN
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IPR000095; PAKbox/Rhobndng.
IPR002290; Ser_thr_pkinase.
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PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
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Pred. No. 4.7e-32;
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STANDARD;

545

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Phosphorylation.
DOMAIN 75
DOMAIN 134
DOMAIN 270
NP_BIND 276
BINDING 299
ACT_SITE 389
MUTAGEN 107
CONFLICT 26
CONFLICT 27
CONFLICT 379
CONFLICT 503
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                            SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
SMART; PS50108; CRIB; 1
PROSITE; PS50107; PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96398842; PubMed=8805275;
Brown J.L., Stowers L., Baer M., Trejo J.,
"Human Ste20 homologue hPAK1 links GTPases
                                                                                                                                                                                                                                                         Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
                                                                                                                                                                                                                                                                                InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000095; PAKbox/Rhobndng.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=97199447; PubMed=9395435;
                                                                                                                                                            Transferase;
                                                                                                                                                                       PROSITE; PS001
                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                               ProDom; PD000001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mammalian cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sells M.A., Knaus U.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated
kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK).
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FUNCTION: THE ACTIVATED KINASE ACTS ON A VINCTION: THE ACTIVATED KINASE ACTS ON A VINCTION THE THE GTPASE EFFECTOR THAT LINK GTPASES TO THE JNK MAP KINASE PATHWAY.

SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND CDC42/P21 AND RAC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a collab
ween the Swiss Institute of Bioinformatics and the EMBL outsi
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY SIMILARITY: BELONGS TO THE SER/THR FAMILY
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                                                                                                                                                           Serine/threonine-protein kinase;
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AAC50590.1;
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                                                                                                                                                           PROTEIN_KINASE_DOM; 1.
PROTEIN_KINASE_ST; 1.
ne/threon:no---
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 60661
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LINKER.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

L->F: CONSTIPUTIVELY A

V -> A (IN REF. 2).

F -> S (IN REF. 2).

D -> E (IN REF. 2).
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 14A1E70E6480CD7E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ambrose
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LINKS THE F
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                                                                                                                                                         ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF PROTEIN KINASES
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Best Local Similarity
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Submitted (AUG-1995) to the EMBL/Genpart S.
                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEAST
                                                                                                                                                                            "Characterization and mute
expressed preferentially
                                                                                                                                                                                                                                                                                                                                                              Friesen H., Lunz R., Submitted (AUG-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sporulation-specific protein 1 (EC SPS1 OR YDR523C OR D9719.27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995
30-MAY-2000
                                                                                                                                           MO1. Cell. Bic -!- FUNCTION:
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P08458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPS1_YEAST
                                                                   between
                                                                                                                                                                  cerevisiae."
                                                                                                                                                                                                    Percival-Smith A., Segall J.;
                                                                                                                                                                                                                MEDLINE=87064542; PubMed=3023934;
                                                                                                                                                                                                                              SEQUENCE OF 396-490 FROM
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                                                       ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                  DEVELOPMENT.
SIMILARITY:
                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
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                                                                                                       SUBFAMILY
                                                                                                                                                     Biol.
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(Rel.
(Rel.
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32, Last sequence up
39, Last annotation
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me EMBL/GenBank/DDBJ
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Pred.
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                                                                                                                                         PROTEIN KINASE
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No. 6.9e-32;
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                                                                                                                                          REQUIRED
                                                                                                                                                                            cluster of three genes
Saccharomyces
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                                                                                                                   PROTEIN
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Petel F.X.,
                                                                                                                                                                                                                                                                                                             Duncan M.,
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                                                                  EMBL
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ST10_HUMAN

ID ST10_HUMAN

AC 094804; 09U

DT 16-CCT-2001

DT 16-CCT-2001

DT 16-CCT-2001

DE kinase).

GN STK10 OR LON

OS HOMO Sapiens

OC Eukaryota; b

OC Mammalia; En

OC Marmalia; En

OC Marmalia; En

OK NCBL_TaxID=

RM [1]

RM SEQUENCE FRO

RM MEDLINE=992

RA Kuramochi SE

RA Tamunogeneti

RU Immunogeneti

RU [1]

RP SEQUENCE OF
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Best Local Similarity
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EMBL; U33057; AAB649
EMBL; M13629; AAA350
PIR; B25376; B25376.
SGD; S0002931; SPS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                 094804; 09UIW4;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                             mouse, and rat h
                                                                                                                     SEQUENCE FROM N.A. MEDLINE=99216434; Pubr
Kuramochi S., Matsuda
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                           STK10 OR LOK.
                                                                                                                                                                                                                                                                       Serine/threonine-protein
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SMART; SM00220; S_TKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                           Homo sapiens (Human)
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                                                mouse, and rat
Immunogenetics
                                                                                         Molecular cloning of the human gene STK10 encoding lymphocyte-
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PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
PS50011; PROTEIN_KINASE_DOM; 1.
                     OF
F
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18 272
24 32
47 47
141 141
454 454
469 469
490 AA; 557
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; AAB64963.1;
; AAA35079.1;
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AAB64963.
                                                49:369-375(1999)
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                                                               homologues
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                        and comparative
                                                                                                                                     PubMed=10199912;
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                                                                                                                                                                                                                                                                       kinase 10
                                                                                                                     Okamoto
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ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
N -> NVN (IN REF. 2).
G -> R (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 489.5;
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6143055E85BAF4FF CRC64;
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                                                                           chromosomal mapping
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                                                                                                                                                                                                                                                                                                                                               968
                                                                                                                     Kitamura
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                                                                                                                                                                                              Hominidae;
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                                                                                                                     Yonekawa
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Best Local
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DOMAIN 36 294
DOMAIN 573 947
DOMAIN 750 884
NP_BIND 42 50
BINDING 65 65
BCT_SITE 157 157
SEQUENCE 968 AA; 112134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0109; TYRKINASE.

PRODOM; PD000001; EUK_PKinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB015718; BAA35073.1;
EMBL; AL133081; CAB61400.1;
HSSP; P24941; 1HCL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 603919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bloecker
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267
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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STE20 SUBFAMILY.
                                                       CDHPYIVKLLGAYYHDGKLWIMIEFCPGGAVDAIMLEL-DRGLTEPQIQVVCRQMLEALN
                                                                                                                                                                                                         LRHPNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKPLQEVEIAAVTHGALQGLA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outsi European Bioinformatics Institute. There are no restrictions
FRDFLKIALDKNPETRPSAAQLLEHPFV
                           FRNFVDSCLQKIPQDRPTSEVLLKHRFV
                                                                                                                   FLHSKRIIHRDLKAGNVLMTLEGDIRLADFGVSAKNLKTLQKRDSFIGTPYWMAPEVVMC
                                                                                                                                             YLHSHNMIHRDVKAGNILLSEPGLVKLGDFG----SASIMAPANSFVGTPYWMAPEVIL-
                                                                                                                                                                                                                                                                  DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
                                                                                                                                                                                                                                       DPNEVWEIVGELGDGAFGKVYKA---KNKETGALAAAKVIETKSEEELEDYIVEIEILAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGNC:11388; STK10
                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boecher M., Brandt P., Mewes H.-W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pkinase;
                                                                                                                                                                                                                                                                                                                                                           112134 MW;
                                                                                                                                                                                                                                                                                                              34.1%; 38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               coil.
                                                                                                                                                                                                                                                                                                54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN KINASE.
COILED COIL (PO'GLN-RICH.
                                                                                                                                                                                                                                                                                                              Score 487.5; DB 1;
Pred. No. 2.1e-31;
                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                           15E245193ECC553D CRC64;
294
                           267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gassenhuber J.,
                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                            968;
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                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANS
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                                                                                                                                                                                                                                                                                               Gaps
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commercial
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                                                                                                                    206
                                                                                                                                                181
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RESULT 12 ST10\_MOUSE ID ST10\_MOUSE

STANDARD;

PRT;

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Best Local S
Matches 105
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16-0CT-2001
                                                                                                                                                                                                                                         ACT_SITE SEQUENCE
                                                                                                                                                                                                                                                                       NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:1099439; Stk10.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predominantly in lymphocytes.";
J. Biol. Chem. 272:22679-22684(1997).
-!- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN HISTONE IIA ON SERINE AND THREONINE RESIDUES.
-!- CAPALYTIC ACTIVITY: ATP + a protecin = ADP + a phosphoprotein.
-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGAN.
-!- TISSUE SPECIFICITY: BYPERESSED PREDOMINANTLY IN LYMPHOID ORGAN.
SUCH AS SPLEEN, THYMUS, AND BONE MARROW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the support of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKc; 1.
PROSTTE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSTTE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                 Phosphorylation; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                 Transterase;
                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D89728; BAA24073.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Karasuyama H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kuramochi S., Moriguchi T., Kuida K.; Endo J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97426413; PubMed=9278426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STK10 OR LOK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine/threonine-protein
                                                              88
                                                                                           69
                                                                                                                       31
                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: AUTOPHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STE20 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES
                                                                           LRHPNTIQYRGCYLREHTAWLVMEYCLGSASD--LLEVHKKPLQEVEIAAVTHGALQGLA 126
                                                                                                                                        DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
FLHGKRIIHRDLKAGNVLMTLEGDIRLADFGVSAKNLKTLQKRDSFIGTPYWMAPEVVLC
                             YLHSHNMIHRDVKAGNILLSEPGLVKLGDFG----SASIMAPANSFVGTPYWMAPEVIL-
                                                          CDHPYIVKLLGAYYYDGKLWIMIEFCPGGAVDAIMLEL-DRGLTEPQIQVVCRQMLEALN 146
                                                                                                                       DPNDVWEIVGELGDGAFGKVYKA---KNKETGALAAAKVIETKSEEELEDYIVEIEILAT 87
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a novel mouse STE20-like protein kinase that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 40, Last annotation
onine-protein kinase 10 (EC
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                             Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                           111992
                                                                                                                                                                                               34.1%; 38.9%;
                                                                                                                                                                                                                                            MW.
                                                                                                                                                                               52;
                                                                                                                                                                                                                                                         COILED COIL (POTENTIAL).
GLN-RICH.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                               Score 486.5;
Pred. No. 2.6e
52; Mismatches
                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; E
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tation update)
10 (EC 2.7.1.37) (Lymphocyte-oriented
                                                                                                                                                                                                                                         SIMILARITY.
7115EAC01032BF94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                              2.6e-31;
nes 100;
                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                            Length
                                                                                                                                                                               Indels
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
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RESULT 13
PAK3_HUMAN
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                                                                                                                                                                                                                                                                                                                                             PAK3_HUMAN
075914;
 DOMAIN
DOMAIN
                                                  ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00288; PBD; 1.
SMART; SM00280; S.TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS500107; PROTEIN_KINASE_ATP; PROSITE; PS50011, PROTEIN_KINASE_DOM; PROSITE; PS00108; PROTEIN_KINASE_ST; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3).
                           Transferase; Serine/threouthe
SH3-binding; Phosphorylation.
                                                                                                                                                                                                       EMBL; AF068864;
HSSP; P24941; 10
                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                              Pfam; PF00786;
                                                                                                                                        Pfam; PF00069;
                                                                                                                                                                                    MIM; 300142;
                                                                                                                                                                                             Genew;
                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAK3 OR OPHN3
                      DOMAIN
                                                                                                                                                             InterPro;
                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98400251; PubMed=9731525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                         STE20 SUBFAMILY.
SIMILARITY: CONTAINS 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRDFLKIALDKNPETRPSAAQLLQHPFVSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEY
                                                                                                                                                                                           HGNC:8592; PAK3
                                                                                                                                       IPR000095; PAKbox/Rhobndng.
IPR002290; Ser_thr_pkinase.
0069; pkinase; 1.
                                                                                                                                                            IPR000719;
IPR000095;
 70
129
268
                                       Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human).
                                                                                                                             pkinase;
PBD; 1.
                                                                                                                                                                                                        1CKP.
                                                                                                                                                                                                                  AAC36097.1;
 267
519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
                                                                                                                                                                     Euk_pkinase
                                                                                                                                                                                                                                                                                                                            CRIB DOMAIN.
          LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269
KINASE
                                          kinase;
                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
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                                         ATP-binding
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Best Local :
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               use by modified
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
kinase 3) (PAK-3) (Beta-PAK) (P65-PAK).
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SEQUENCE
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                                                                                                                                                                                                                                                                           J. Biol.
                                                       between
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                                                                                                                                                                                                                                                                                      kinase (PAK) family.
                                                                                                                                                                                                                                                                                                                                             MEDLINE=96027610;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND
                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAK3_RAT
                                                                                                                                                                                                                                                                                                                                Manser E., Chong
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                     Molecular cloning of a new member of the p21-Cdc42/Rac-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                          Biol. Chem. 270:25070-250/8(1595).

FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.

FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.

SUBURIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND

CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3

DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK (
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                        PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED SIMILARITY: BELONGS TO THE SER/THR FAM:
                                                                                                                                                                  LOW LEVELS IN THE TESTIS.
DEVELOPMENTAL STAGE: FOUR
                                                                                                                                                                                             SIMILARITY)
TISSUE SPEC
                                                                                              SIMILARITY: CONTAINS 1 CRIB
                                                                                                                                                    EXPRESSION ELSEWHERE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLNRCLEMDVDRRGSAKELLQHPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQS-GHWSEYFRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS - - - FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRHPNTIQYRGCYLREHTAWLVMEYCL-GSASDLLEVHKKPLQEVEIAAVTHGALQGLAY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DPKKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNL---QQQPKKELIINEILVMRE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVDSCLQKIPQDRPTSEVLLKHRFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                            SUBFAMILY.
                                                                                                                                                                                           SPECIFICITY: DETECTED AT HIGH
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297
387
544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                             PubMed=7559638;
C., Zhao Z.-S.,
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297
387
60692
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41.9%;
                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE
                                                                                                                                                                 FOUND IN THE
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ATP
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519
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P (BY SIMILARITY).
SIMILARITY.
                                                                                                DOMAIN.
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                                                                                                                                                                  EMBRYONIC
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FAMILY OF PROTEIN KINASES
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                                                                                                                                                                                                                                                                                                                                                                                                              Muridae;
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                                                                                                                                                                 CNS
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; Murinae; Rat
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RESULT 15
PAK3_MOUSE
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Best Local
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DOMAIN 70
DOMAIN 129
DOMAIN 268
NP_BIND 274
    TISSUE=Fibroblast;
MEDLINE=96032693; PubMed=7559398;
MEDLINE=96032693; PubMed=7559398;
Bagrodia S., Taylor S.J., Creasy C.L., C
"Identification of a mouse p21Cdc42/Rac
"Identification of a mouse p21Cdc42/Rac
J. Biol. Chem. 270:22731-22737(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
PROSITE;
                                                                                                                                                  Q61036; O88645;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-)
kinase 3) (PAK-3) (Beta-PAK) (CDC42/RAC effector k
                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                             Mus musculus (Mouse)
                                                                                                                                          PAK3 OR PAK-3 OR STK4 OR PAKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000001; Euk_pki
SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; Pfam; PF00786; PBD; 1.
[2]
                                                                     SEQUENCE
                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                           PAK3_MOUSE
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HSSP; P24941;
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                                                                                                                                                                                                                                                                                                                                                                                            LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM
                                                                                                                                                                                                                                                                                                                                                                                                                             NKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDV--VTETCMDEGQIAAVCRECLQALDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPKKKYTRFEKIGQGASGTVYTALDIATGQEVAIKQMNL---QQQPKKELIINEILVMRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
                                                                                                                                                                                                                                                                                     FLNRCLEMDVDRRGSAKELLQHPFL
                                                                                                                                                                                                                                                                                                          FVDSCLQKIPQDRPTSEVLLKHRFV
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                                                                                                                                                                                                                                                                                                                                   TRKAYGPKVDIWSLGIMAIEMVEGEPPYLNENPLRALYLIATNGTPELQNPERLSAVFRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
111; Conser
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                                                                     FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPRO00095; PAKbox/n......IPR002290; Ser_thr_pkinase.
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IPR000095; PAKbox/Rhobndng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN_KINASE_ATP;
PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euk_pkinase;
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46; Mismatches
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 484; DB 1;
Pred. No. 2.1e-31
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                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                     519
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                    Chernoff J. c activated
                                                                                                                                                                                                                          A
                                                                                                      Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 544;
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                                                                                                                                                      kinase
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                       Cerione inase.";
                                                                                                                 Euteleostomi;
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SMART; SM00285; PBD; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bagrodia .
J. Biol. (
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CONFLICT
CONFLICT
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000095; Pakbox/Rhobndng.
InterPro; IPR00290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF00786; PBD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Burbelo P.D., Kozak C.A., Finegold A.A., Hall A., Pirone D.M.;
"Cloning, central nervous system expression and chromosomal manufacture mouse PAK-1 and PAK-3 genes.";
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                 LHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANS----FVGTPYWMAPEVILAM 183
                                                                                                                                                                      DPKKKYTRLEKIGQGASGTVYTALDIATGQEVAIKQMNL---QQQPKKELIINEILVMRE 319
                                                                                                                                                                                                             DPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDIIKEVRFLQK 68
LHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVV---
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                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                    544 AA;
                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation.
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267
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G -> A (IN REF
V -> E (IN REF
H -> R (IN REF
L -> M (IN REF
                                                                                                                                                                                                                                                                                  Score 480; DB 1;
Pred. No. 4.3e-31;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                    C4AEB71DD33E6988 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                        REF.
REF.
                                                                                                                                                                                                                                                              95;
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Post-processing: Minimum Match 0%
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                          Database :
          SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inwan:*
5: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
11: sp_rodent:
12: sp_virus:*
13: sp_vertebra
14: sp_unclass:
15: sp_urclass:
16: sp_bacteria:
17: sp_archeap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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1428
1 VABELFFKDDPEKLFSDLREI.........PQDRPTSEVLLKHRFVLRER 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        November 22, 2002, 12:20:50; Search time 15.0405 Seconds (without alignments) 3712.561 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
sp_organelle:*
sp_phage:*
sp_plant:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                                                                                                   sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                    sp_invertebrate:*
sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	DВ	ID	Description
1	1428	100.0	1235	11 1 11 1	Q9JLS3	Q9jls3 rattus norv
2	1424	99.7	1049	4	094957	094957 homo sapien
ω	1424	99.7	1235	4	Q9UL54	Q9ul54 homo sapien
4	1316	92.2	1001	11	088664	088664 rattus norv
ഗ	1314	92.0	1005	4	Q9P2I6	Q9p2i6 homo sapien
6	1306	91.5	1001	4	Q9H2K7	Q9h2k7 homo sapien
7	1211	84.8	898	4	Q9UHG7	Q9uhg7 homo sapien
8	1211	84.8	898	4	Q9нс79	Q9hc79 homo sapien
9	1210	84.7	898	13	Q919E0	Q9i9eO gallus gall
10	1208	84.6	898	4	Q9NZM9	Q9nzm9 homo sapien
11	1202	84.2	868	4	Q9H2K8	Q9h2k8 homo sapien
12	1086	76.1	1039	σ	Q9VWG8	Q9vwg8 drosophila
13	631.5	44.2	836	10	024527	024527 arabidopsis
14	631.5	44.2	842	10	Q9FNU3	
15	631.5	44.2	1120	10	Q9LQA1	
16	609.5	42.7	825	10	Q9ARL7	~

	45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
	(.)	(+)	141	1.3	537.5	(4)	538	539	539	541	541	541	543	544	550	550	550	550	550	550	555	555	557.5	557.5	568.5	572	586.5	604	608.5
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	1331	1323	1305	1297	1276	1268	491	653	651	497	491	445	478	398	640	525	523	497	487	421	669	596	416	416	426	461	431	809	825
	4	4	4	4	4	4	4	ഗ	σı	11						σı	ഗ	σı	11	σı	Ģ	σ	11	4					
,	O9UKE4	Q9UKEO	Q9UKE3	09UKD9	Q9UKE1	Q9UKD8	Q96FM6	Q22553	Q95ZN6	Q9JI10	054748	Q60877	062571	Q9H7S5	Q95ZM6	Q966K8	Q966K9	Q9NB31	Q9JI11	Q95ZM5	Q8T0S6	Q9V8W4	Q99JT2	Q9P289	Q96BA2	061125	Q99КН8	Q8VYC1	Q8SAE1
	homo	homo	homo	homo	homo	homo	Q96fm6 homo sapien		caen	Q9ji10 mus musculu	O54748 rattus norv	Q60877 mus musculu		Q9h7s5 homo sapien	Q95zm6 caenorhabdi	Q966k8 caenorhabdi	_	Q9nb31 caenorhabdi	Q9jill mus musculu			rosc	Sun	homo	Q96ba2 homo sapien	O61125 dictyosteli		Q8vycl arabidopsis	Q8sael triticum mo

## ALIGNMENTS

RR RP CC	RESULT RE
SEQUENCE FROM N.A.  Chen Z., Hutchison M., Cobb M.;  Chen Z., Hutchison M., Cobb M.;  Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.  -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  EMBL; AF140556; AAD39480.2;  HSSP; P24941; 1B38.  InterPro; IPR001099; Gram_pos_anchor.  InterPro; IPR001099; Gram_pos_anchor.  InterPro; IPR0010906; Ig_MHC.  InterPro; IPR0012290; Ser_thr_pkinase.  InterPro; IPR001245; Tyr_pkinase.  InterPro; IPR00109; TYRKNASE.  PRODOm; PD000001; EWk_pkinase; 1.  PRINTS; PR00109; TYRKNASE.  PROSITE; PS00343; GRAML POS_ANCHORING; UNKNOWN_1.  PROSITE; PS00343; GRAMLPOS_ANCHORING; UNKNOWN_1.	ATS OUT

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RESULT
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DR
SQ
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                                                                                           "Characterization of a Subfamily of Human STE20-like King Selectively Activate p38 Through MKK3 and are Regulated v dependent Mechanism.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL; AB020688; BAA74904.1; -.
EMBL; AF263313; AAG38503.1; -.
HSSP; P24941; 1B38.
InterPro: TDBDGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00
PROSITE; PS50
PROSITE; PS00
ATP-binding;
SEQUENCE 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             094957;
                                                                                                                                                                                                                                                              MEDLINE-99156230; PubMed-10048485;
Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotuani H., Nomura N., Ohara O.,
"Prediction of the coding sequences of unidentified human
The complete sequences of 100 new cDNA clones from brain w
for large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
PROSITE;
            Pfam, PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE,
Probom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
                                                              InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                               KIAA0881
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TREMBLrel. 10, Created)
01-MAY-1999 (TREMBLrel. 10, Last sequence up
01-MAR-2002 (TREMBLrel. 20, Last annotation
KIAA0881 protein (STE20-like kinase).
                                                                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALQGLAYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYWMAPEVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEVRFLQKLRHPNTIQYRGCYLREHTAWLYMEYCLGSASDLLEVHKKPLQEVEIAAVTHG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS00107; PROTEIN_KINASE_ATP; 1.
PS00101; PROTEIN_KINASE_DOM; 1.
PS00108; PROTEIN_KINASE_T; 1.
ing; Kinase; Serine/threonine-protein kinase; Transferase.
1235 AA; 138750 MW; 426960D0812518AD CRC64;
PS00107;
                                                                                                                                                                                                                                                         5:355-364(1998).
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PROTEIN_KINASE_ATP;
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Pred. No. 8.3
0; Mismatches
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Catarrhini;
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i; Hominidae;
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Query Match
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Q9UL54;
01-MAY-2000 (TrEMBLrel. 13, C)
01-MAY-2000 (TrEMBLrel. 13, Lz
01-MAY-2002 (TrEMBLrel. 20, Lz
Prostate derived STE20-like k
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PROSITE; PS00108
ATP-binding; Kind
SEQUENCE 1049
                                                                                                                                 Pfam; PF00069; pkinase; 1.

PRINTS; PR00109; TYRKINASE.

PTODOM; PD000001; EUK_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                    organisation.";
J. Biol. Chem. 275:4311-4322(2000)
--- SIMILARITY: BELONGS TO THE SER
EMBL; AF061943; AAD45616.1; --
HSSP; P24941; 1B38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=BREAST CARCINOMA;
MEDLINE=20127920; PubMed
                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                          InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morris J.D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moore T.M., Garg R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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Local Similarity
mes 270; Conserv
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                                                                                             Kinase; Serine/threonine-protein kinase;
235 AA; 138232 MW; 3AB9E8E690934307 CRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CINOMA;
PubMed=10660600;
Thrson C., Coptcoat M.J.,
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PROTEIN_KINASE_ST; 1.
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Best Local
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SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00110; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-prosequence 1001 AA; 115952 MW; 85511B62
                                                                                                                                                                                                                                                                                                                                                                                                     Hutchison M., Berman K.S., Cobb M.H.;
"Isolation of TAO1, a protein kinase that activates activated protein kinase cascades.";
J. Biol. Chem. 273:28625-28632(1998).
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROEMBL; AF084205; AAC71014.1; -.
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01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Serine/threonine protein kinase TAO1.
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01-NOV-1998
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
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                                                 KEVRFLOKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLOEVEIAAVTHG
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Pred. No. 9.
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InterPro; IPR002299; Ser_thr_pkinase.
InterPro; IPR002299; Ser_thr_pkinase.
Pfam; PF000069; pkinase; 1.
PRINTS; PR000109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
PROSITE; PS000101; PROTEIN_KINASE_ATP; 1.
PROSITE; PS000108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS000108; PROTEIN_KINASE_ST; 1.
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Homo sapiens (Human).
'Tronta; Metazoa; Chordata; delication (Human).
'Tronta; Metazoa; Primates;
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-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL; AB037782; BAA92599.1; -.
EMBL; AY049015; AAL12217.1; -.
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Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes
The complete sequences of 150 new cDNA clones from brain which
for large proteins in vitro.";
DNA Res. 7:65-73(2000).
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"Characterization of human TAO1.";
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                                  RNFVDSCLQKIPQDRPTSEVLLKHRFVLRER
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                                                                                                                                                                                                                                                                                    ALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVGTPYWMAPEVI
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116540 MW;
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289
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Best Local S
Matches 242
                                                                                             O9UHG7
O9UHG7:
O9UHG7:
O1-MAY-2000 (TrEMBLrel. 1
O1-MAY-2000 (TrEMBLrel. 1
O1-MAR-2002 (TrEMBLrel. 2
              JIK.
Homo sapiens (Human).
Hotocoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yustein J.T., Robinson D., Kung H.-J.;
"Characterization of a Subfamily of Human Selectively Activate p38 Through MKK3 and dependent Mechanism.";
Submitted (MAY-2000) to the EMBL/GenBank/DEMBL; AF263312; AAG38502.1; -.
                                                                                   STE20-like
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Probom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TRC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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Mammalia; Eutheria;
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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Primates;
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16, Last sequence update)
21, Last annotation update)
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                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                           Created)
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Pred. No. 7.6e-110;
7; Mismatches 12;
                      Craniata;
                                                                                                                                                                                    PRT;
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Catarrhini;
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i; Hominidae; Homo.
                      Vertebrata;
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                      Euteleostomi;
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Best Local Similarity
                 SEQUENCE FROM N.A.

MEDITINE=20384190; PubMed=10924369;

Zhang W., Chen T., Wan T., He L., Li N., Yuan Z., Cao X.

"Cloning of DPK, a novel dendritic cell-derived protein activating the ERK1/ERK2 and JNK/SAPK pathways.";

Biochem. Biophys. Res. Commun. 274:872-879(2000).
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;
                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created 01-MAR-2001 (TrEMBLrel. 16, Last so 01-JUN-2002 (TrEMBLrel. 21, Last ar Serine kinase (STE20-like kinase).
                                                                                                                                                                                         Q9HC79
Q9HC79;
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SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 898 AA; 105657 MW; 61F04628713E6025 CRC64;
SEQUENCE
                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_th_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000130; Zn_MTpeptdse.
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PRINTS; PR00109; TYRKINASE.
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Best Local Similarity
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InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001210; Zn_MTpeptdse.
InterPro; IPR001130; Zn_MTpeptdse.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PrODom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; TyrKC; 1.
SMART; SM002219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
ATP-binding; Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/Ge
EMBL; BR135158; AAG09131.1; -
EMBL; BC002756; AAH02756.1; -
EMBL; BC002756; AAH02756.1; -
HSSS; P24941; 1B38
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0002290; Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q919E0
Q919E0;
01-OCT-2000 (TremBLrel. 1
01-OCT-2000 (TremBLrel. 1
01-MAR-2002 (TremBLrel. 2
                                                                                        activate the SAPK/JNK pathway.";
Oncogene 19:710-718(2000).
EMBL; AF263314; AAF73045.1; -.
HSSP; P24941; 1B38.
                                                                                                                                                                              MEDLINE-20162342; PubMed-10698516;
Yustein J.T., Li D., Robinson D., Kung H.
"KFC, a Ste20-like kinase with mitogenic
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                      InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
InterPro; IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                       Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=PLACENTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                            (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMDEGOYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRFVDYCLQKIPQERPTSAELLRHDFVRRDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAITHG
                                                                                                                                                                                                                                                                                                                                                                        gallus (Chicken).
ota: Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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Pred. No. 2.8e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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1es 22;
                                                                                                                                                                                                           .J.;
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                                                                                                                                                                                   capability
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Interpro; IPR000130; 2000.

R Pfam; PF00069; pkinase; 1.

R PRINTS; PR00109; TYRKINASE.

R ProDom; PD000001; Euk_pkinase; 1.

JR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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Q9NZM9
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Best Local S
Matches 222
Query Match
Best Local Similarity
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Q9NZM9;
01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                           Carter T.G., Benton B., Fruhling D., Monks C.R.F., Windm Kupfer A., Manfredi J., Johnson G.L., Pleiman C.M.;

"KDS and TAO1, two related proteins with kinase domain b STE20, differentially relocate in mitogen stimulated T 1 submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.

-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN EMBL, AP181985, AAF25817.1;

EMBL; AP181985, AAF25817.1;

HSSP; P24941; 1B38.
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

NON_TER 898 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                            IPR000719; Euk_pkinase.
IPR002290; Ser_thr_pkinase.
IPR001245; Tyr_pkinase.
IPR000130; Zn_MTpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 15, ) (TrEMBLrel. 15, 2) (TrEMBLrel. 20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Last
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    Score
Pred.
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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    1208;
No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 898
       DB 4;
.3e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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Best Local S
Matches 219
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Q9H2K8;
Q1-MAR-2001
Q1-MAR-2001
Q1-JUN-2002
                                                                                                                                                                                                                                                                                       Kinase.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yustein J.T., Robinson D., Kung H.-J.; "Characterization of a Subfamily of Human Selectively Activate p38 Through MKK3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STE20-like kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; 1. PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR000130; Zn_MTpeptdse.
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                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                             -
                                                                                         sapiens (Human)
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KEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAITHG
                                          KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNFVDSCLQKIPQDRPTSEVLLKHRFVLRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF
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tted (MAY-2000) to the EMBL/GenBank/DDBJ databases AF263311; AAG38501.1; -.

P24941; 1B38.
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                                                                                                                                                                                            l Similarity
219; Conser
                                                                                                                                                                                                                                                                                                                                                             PS00107; PROTEIN_KINASE_ATP; 1.
PS50011; PROTEIN_KINASE_DOM; 1.
PS00108; PROTEIN_KINASE_ST; 1.
PS00142; ZINC_PROTEASE; UNKNOWN_1
                                                                                                                                                                                                                                                                                       898
868
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                          898 ·
105501 MW;
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80.8%;
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                                                                                                                                                                                         Score 1202; DB 4;
Pred. No. 1.9e-100;
8; Mismatches 24;
                                                                                                                                                                                                                                                                                       E52C5BFEDD67264E CRC64;
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                                                                                                                                                                                                                                        Length
                                                                                                                                                                                            Indels
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                                                                                         RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.E., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson K.A., Nixon K., Nusskern D.R., Paeleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paeleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Wapers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
DR KMIL ARD0357.2 Aarafag7a 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris M. Kallsh F. Karnen G. H. K.F., Kerpingen J.A. Kerphum K.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9VWG8 PRELIMINARY:
Q9VWG8:
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG14217 protein.
CG14217.
                                                                               EMBL; AE003512; AAF48973.1;
                                                    HSSP; P24941; 1B38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRFVDYCLQKIPQERPTSAELLRHDFVRRDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNFVDSCLQKIPQDRPTSEVLLKHRFVLRER 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF
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FBgn0031030; CG14217.
; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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13,
20,
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Last annotation update)
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                                                                                                                                                                                   Q., Zheng L.,
X., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K.A.,
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Best I
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                       Pfam; PF00069; pkinase; 1.

ProDom; PD00001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP;

PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thaliana chromosome I BAC F23010 genomic sequence."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; 096313, AAB68776.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20,
                                                                               InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase
Pfam: PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                  STRAIN=CV. COLUMBIA; Winge P., Brembu T., Submitted (APR-1997)
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine kinase. SIK1 OR F23010.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              024527;
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS50011; PROTEIN_KINASE_DOM; ATP-binding; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          024527
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SMART; SM00220; S_TKc; 1.
  SEQUENCE
            ATP-binding;
                                                                                                                      HSSP; Q00534; 1BI8.
                                                                                                                                                                                                                              STRAIN=CV.
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002290; Ser_thr_pkinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSFVELCLKKMPAERPSSAKLLTHAYVTRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNFVDSCLQKIPQDRPTSEVLLKHRFVLRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGHWSEYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLSGLSYLHSLGRIHRDIKAGNILLTDNGVVKLADFGSAAIKCPANSFVGTPYWMAPEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEVRFLQKLRHPNTIQYRGCYLREHTAWLVMEYCLGSASDLLEVHKKPLQEVEIAAVTHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IADLFNKHDPEKIFEDLREIGHGSFGAVYYARCNLTREIVAIKKMSYTGKQSQEKWQDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAMDEGQYDGKVDVWSLGITCIELAERKPPYFNMNAMSALYHIAQNESPTLPKNDWSDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEIRFLRQLNHPNTIEYKGCYLRESTAWLVMEYCVGSASDIIEVHKKPLHEDEIAAICLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                             COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1039 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
           Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pkinase;
  92721 MW;
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74.28;
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           Transferase
                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                   Bones A.M.
                                                                                                                                                                                                                                                                                              TISSUE=HYPOCOTYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
805F18FDFA430762 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391D15216D295F3A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                Wu D.,
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RESULT
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Best Local (
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Best Local :
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Q9FNU3;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                   Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase;
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYTKC; 1.
                                                                                                                                                                                                                                                                                            Plant Physiol. 125:1342-1353(2001).
EMBL; AY013245; AAG45491.1; -.
HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                "Comparative sequence analysis of colinear barley artificial chromosomes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                   PROSTIE; PS00107; PROTEIN KINASE_ATP;
PROSTIE; PS50011; PROTEIN KINASE_DOM;
ATP-binding; Transferase.
SEQUENCE 842 AA; 91646 MW; EBE222:
                                                                                                                                                                                                                                                                                                                                                            Dubcovsky J., Ramakrishna W. Shiloff B.A., Bennetzen J.L.
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21140318; PubMed=11244114;
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3615.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4530;
                                                                                                                                                                                                                                                       InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkin
InterPro; IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242
306 GEIEMLQQCSHPNVVRYFGSYQGEEYLWIVMEYCGGGSVADLIGITEEPLDESQIAYICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity nes 127; Conserv
                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                              1 VAELFFKDDPEKLFSDLREIGHGSFGAVYFARDVRNSEVVAIKKMSYSGKQSNEKWQDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNFVDSCLQKIPQDRPTSEVLLKHRFVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VPESVTREDPSTKYELLHELGKGSYGAVYKARDLRTQELVAIKIISLT--EGEEGYEDIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDFVAKCLTKEPRLRPTAAEMLKHKFVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --QENRYDGKVDVWALGVSAIEMAEGLPPRSSVHPMRVLFMISIEPAPMLEDKEKWSLVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQNESPALQSGH-WSEYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYLHSIYKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSAS----IMAPANSFVGTPYWMAPEVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REDPTTKYEFLNELGKGSYGSVYKARDLKTSEIVAVKVISLT--EGEEGYEEIRGEIEML
                                                                                                   al Similarity
127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  NIPPONBARE; TRANSPOSON=GAIGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                               44.2%;
46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.2%; score 631.5; DB 10
47.2%; Pred. No. 1.2e-48;
tive 54; Mismatches 77;
                                                                                                                                                                                                                                                                   Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                                                        W., SanMiguel P.J.,
                                                                                                   52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                                                                                                                 Pred.
                                                                                                                           Score 631.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                     EBE222157E40558C CRC64;
                                                                                                  Mismatches
                                                                                                                 No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Embryophyta; Tracheophyta; a; Poales; Poaceae;
                                                                                                   ..3e-48;
les 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
                                                                                                                           DB 10;
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RESULT 15
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01-CCT-2000 (TrEMBLrel. 1
01-CCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
F4N2.17.
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SMAAT; SM00220; S_TKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
ATP-binding; Transferase.
SEQUENCE 1120 AA; 124623 MW; 9B3881B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Kim Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000504; RNA_rec_mot.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR0069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AC008262; AAI
HSSP; Q00534; 1BI8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases. EMBL; ACC08262; AAF27066.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic sequence for Arabidopsis thaliana BAC F4N2 from I.";
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                             241 RNFVDSCLQKIPQDRPTSEVLLKHRFVLR 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 44.2%; Sou Local Similarity 47.2%; Proceedings of the conservative 54;
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                                                                                                                                                                                                                              QKLRHPNTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVEIAAVTHGALQGL 125
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                                                                                    --QENRYDGKVDVWALGVSAIEMAEGLPPRSSVHPMRVLFMISIEPAPMLEDKEKWSLVF
                                                                                                                                                                                                                                                                                                                                                                                                                              REDPTTKYEFLNELGKGSYGSVYKARDLKTSEIVAVKVISLT--EGEEGYEEIRGEIEML 299
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                                                                                                                                                                                             AYLHSIYKVHRDIKGGNILLTEQGEVKLGDFGVAAQLTRTMSKRNTFIGTPHWMAPEVI-
                                                                                                                                                                                                                                                                                                             QQCNHPNVVRYLGSYQGEDYLWIVMEYCGGGSVADLMNVTEEALEEYQIAYICREALKGL
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Pred. No. 1.9e-48;
""amatches 77; Indels
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Db 477 HDFVAKCLTKEPRLRPTAAEMLKHKFVER 505

Search completed: November 22, 2002, 12:26:22 Job time: 19.0405 secs